Case Packet

United States v. Dzhokhar Tsarnaev

December 18, 2014

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Cybergenetics

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Documentation of information pertaining to case chain of custody, planning, processing, and reporting as well as citations of populations used.

Notes

The case notes show the organization and processing of a case. Chain of custody information, results, and observations are also included.

Cybergenetics

Boston

Home | Massachusetts State Police

Administrative

CYB name: Boston
Lab: 13-07864, 13-08091, 13-08140
Victims: Richard Donohue, Jr., Sean Collier, Dun Meng
Suspects: Dzhokhar Tsarnaev, Tamerlan A. Tsarnaev
Other name: Case with relatives
Evidence: Glove interior

CYB Operator: Bill Allan

Report to: Jennifer Montgomery
Forensic Scientist II
DNA Unit/Crime Scene Response Unit
MA State Police Forensic and Technology Center
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Assistant U.S. Attorney William D. Weinreb
United States Attorney's Office
John Joseph Moakley Federal Courthouse
1 Courthouse Way
Suite 900
Boston, MA 02210
617-748-3222
Fax: 617-748-3358
Email: william.weinreb@usdoj.gov

Chain of Custody
Sender: Jennifer Montgomery
Organization: MA State Police Forensic and Technology Center
Date: 23 Oct 2014
Time: 11AM
Mode: multiple email messages
K data.rtf
Brother #2.rtf
Questioned item data (10sec).rtf
Questioned item data (20 sec).rtf
Receiver: Bill Allan
Description: Sequencer .fsa files
file_list.txt
Action: copied files to /fileserve/masp/23oct2014;

Lab reports
- Sent by Jennifer Montgomery to Bill Allan on 4 Dec 2014; posted 4 Dec 2014
13-08140.pdf

Case context
- email message received from Jennifer Montgomery on 23 Oct 2014; posted by Bill Allan
RE_ Case with relatives(3).rtf

Data

Evidence
- description from lab report 13-08140.pdf pg 5.

CYB	Item	Description
glove	12-9.5.1	Swab/scrapings of interior palmar side of right glove recovered from driver side front floor area (Honda Civic MA Reg. 116GC7)

- posted 23 Oct 2014 by Bill Allan
glove.jpg
- Lab EPGs received 4 Dec 2014 from Jennifer Montgomery
12-9.5.1.pdf

Reference
- description from lab report 13-08140.pdf pgs 2 and 3.

CYB	Item	Description
DT	12-1.1.1	KBS- Dzhokhar Tsarnaev
TT	15-1.1	KSS- Tamerlan A. Tsarnaev

Population United States FBI Populations
Kit: Identifiler
Sequencer: 3130xl
Software: 3.3.5333.1 (30-May-2014)
Server: 3.25.4441.1

Files

Request
- posted 23 Oct 2014 by Bill Allan
Boston_evi.req
Boston_ref.req
- posted 28 Oct 2014 by Bill Allan
Boston_evi2.req
- posted 5 Nov 2014 by Bill Allan
Boston_evi3.req

Report

- screen - posted 23 Oct 2014 by Bill Allan
Boston_report_screen.txt

Boston_match_screen.xls

- standard - posted 11 Nov 2014 by Bill Allan
  Boston_report.txt
  Boston_match.xls

Notes

23 October 2014, Bill Allan, Obtainer, Planner and Operator
- Received and reviewed the case information.
- Analyzed and uploaded the peak data to system2 World Boston.
- Following review of the data with Jenn Hornyak, proposed the initial requests:

name	n contribs	knowns	degraded	cycles
glove_ncon3_5K	3			5K
glove_ncon4_5K	4			5K
glove_ncon3_dgrd_200K	3		on	200K
glove_ncon4_dgrd_200K	4		on	200K

28 October 2014, Bill Allan, Operator
- Following discussion with Dr. Perlin, replicated initial requests and include new requests assuming reference as known contributor:

name	n contribs	knowns	degraded	cycles
glove_ncon3_dgrd_200K_rep1	3		on	200K
glove+TT_ncon3_dgrd_200K	3	TT	on	200K
glove+TT_ncon3_dgrd_200K_rep1	3	TT	on	200K
glove_ncon4_dgrd_200K_rep1	4		on	200K
glove+TT_ncon4_dgrd_200K	4	TT	on	200K
glove+TT_ncon4_dgrd_200K_rep1	4	TT	on	200K

Preliminary report
- sent by email from Dr. Perlin to Jennifer Montgomery on 5 Nov 2014

Jennifer,

Cybergenetics completed its initial TrueAllele® computer processing on the glove data in your 'case with relatives'. Here are conservative estimates from the preliminary results.

The TrueAllele computer found that a match between the glove interior (Item 12-9.5.1) and Brother #1 (Item 15-1.1, TT) is about ten thousand times more probable than coincidence.

The computer found that a match between the glove interior (Item 12-9.5.1) and Brother #2 (Item 12-1.1.1, DT) is about a thousand times more probable than coincidence.

Based on TrueAllele validation studies, and specificity measurements made on the evidence genotypes in this case, these results are well-separated from statistics for someone who did not contribute their DNA to the

mixture.

Please let me know whether you would like Cybergenetics to confirm these TrueAllele results and prepare a DNA match report. This reporting would take one to two weeks for us to complete.

Thanks. - Mark

5 November 2014, Bill Allan, Operator
- Following discussion with Dr. Perlin, replicated requests and added 5 contributor requests:

name	n contribs	knowns	degraded	cycles
glove+TT_ncon4_dgrd_200K_rep2	4	TT	on	200K
glove_ncon5_dgrd_200K	5		on	200K
glove_ncon5_dgrd_200K_rep1	5		on	200K
glove_ncon5_dgrd_200K_rep2	5		on	200K
glove+TT_ncon5_dgrd_200K	5	TT	on	200K
glove+TT_ncon5_dgrd_200K_rep1	5	TT	on	200K
glove+TT_ncon5_dgrd_200K_rep2	5	TT	on	200K

Report
- draft posted 5 December 2014 by Bill Allan
- final review on 8 December 2014 done by Dr. Mark Perlin
Boston_report.doc

• Data. Peaks mainly between 50 and 1000 rfu.
• Mixture. Consistent with at least 3 contributors (CSF, D21, FGA, TH01), possibly 4 (D3) or 5 (D18).
• Degradation. Some differential degradation between contributors.
• Separation. Better separation when using more contributors.
• Convergence. Good MW convergence, largely with GR < 1.2.

Match to suspect DT

• Genotype inference. Different from the population genotypes, with average KL ~ 4.
• Genotype separation. Similar contributor genotypes, with some probability differences.
• Genotype concordance. Good agreement across 7 independent computer runs.
• Genotype match. Suspect-matching genotype mixture weight = 0.3066 (stdev = 0.1412) & KL = 6.1885.
• Reported match. Representative genotype match to suspect with log(LR) value 4.3824.

Boston 13-08140 evidence MASP glove_ncon5_dgrd_200K_rep1 14 2

glove_ncon5_dgrd_200K_rep1 contrib 2 vs. DT.xls

Match to suspect TT

• Genotype inference. Different from population, with average KL ~ 5.
• Genotype separation. Similar contributor genotypes; some probability differences.
• Genotype concordance. Good agreement between 7 independent computer runs.
• Genotype match. Suspect-matching genotype mixture weight = 0.3039 (stdev = 0.1287) & KL = 6.2119.

• Reported match. Representative genotype match to suspect with log(LR) value 4.8488.

Boston 13-08140 evidence MASP glove_ncon5_dgrd_200K_rep2 19 3

glove_ncon5_dgrd_200K_rep2 contrib 3 vs. TT.xls

Comparison with both suspects DT & TT

• The two references share many alleles, which is consistent with siblings.
• At loci where they share no alleles (TH01), there is support for both genotypes in the data.
• At loci where they share one allele (CSF,D13,D16,D18,D19,D21,D3,D5,D8,TPOX), there is data support for both.
• At loci where the genotypes are the same (D2, D7, FGA, vWA), assuming TT reduces DT probability.
• Their LR's have similar numerical values.

Signed report sent by Dr. Perlin to AUSA Weinreb on 8 Dec 2014
Boston_report.pdf

Document Info

Tags

Related

United States FBI Populations

Citations:

1. Budowle B, Moretti TR, Baumstark AL, Defenbaugh DA, Keys KM. Population data on the thirteen CODIS core short tandem repeat loci in African Americans, U.S. Caucasians, Hispanics, Bahamians, Jamaicans, and Trinidadians. J Forensic Sci 1999;44(6):1277–1286.

2. Budowle B, Shea B, Niezgoda S, Chakraborty R. CODIS STR loci data from 41 sample populations. J Forensic Sci 2001:46;(3):453–489.

3. SEH and SWH counts provided by B. Budowle, FBI Academy.

Data

Quantitative peak data from STR experiments on biological evidence that was entered as input for TrueAllele® computation.

Table

The data table shows the peak information for each evidence item. Each row gives statistics for one peak. The columns describe the peak as:

The DNA template that includes the peak.

The track indicates the amplification(s) included in the template.

The locus that includes the peak.

The peak's designation (i.e., number of repeats).

The base pair length of the peak.

The peak's height in RFU values.

The area under the peak.

Item 12-9.5.1

template	track	locus	desig	length	height	area
1	1	AMELO	0	100.891	13	5
1	1	AMELO	0.1	102.091	32	12
1	1	AMELO	0.2	103.182	13	5
1	1	AMELO	1	106.891	1104	413
1	1	AMELO	1.3	109.4	23	9
1	1	AMELO	1.4	110.6	12	5
1	1	AMELO	2	112.891	489	183
1	1	CSF1PO	8	313	67	38
1	1	CSF1PO	9	316.907	12	7
1	1	CSF1PO	10	321	372	202
1	1	CSF1PO	11	324.905	496	227
1	1	CSF1PO	12	328.899	426	200
1	1	CSF1PO	13	333	381	190
1	1	D13S317	7	213	10	5
1	1	D13S317	8	216.897	538	188
1	1	D13S317	9	221	22	8
1	1	D13S317	10	225	587	230
1	1	D13S317	11	229	859	346
1	1	D13S317	12	233	512	212
1	1	D16S539	9	268	64	27
1	1	D16S539	10	272	433	214
1	1	D16S539	11	275.901	736	315
1	1	D16S539	11.2	278.058	10	6
1	1	D16S539	12	279.903	317	148
1	1	D16S539	13	284	155	71
1	1	D18S51	12	281.906	16	7
1	1	D18S51	13	286	52	22
1	1	D18S51	14	290	481	215
1	1	D18S51	15	293.908	233	99
1	1	D18S51	16	298	58	26
1	1	D18S51	17	301.91	34	15
1	1	D18S51	18	306	53	24
1	1	D18S51	19	310	231	115
1	1	D18S51	20	314	80	35
1	1	D18S51	22	322	26	11
1	1	D18S51	25.2	336.089	11	4
1	1	D18S51	28.1	346.827	13	3
1	1	D19S433	7.1	94.8491	13	1
1	1	D19S433	7.2	95.9919	16	8
1	1	D19S433	12	114	70	27
1	1	D19S433	12.2	116	20	9
1	1	D19S433	13	118	102	40

1	1	D19S433	13.3	120.628	13	6
1	1	D19S433	14	122	1154	430
1	1	D19S433	15	126	592	202
1	1	D19S433	15.2	128	17	8
1	1	D21S11	29	205	70	24
1	1	D21S11	30	209	443	167
1	1	D21S11	30.2	211	89	32
1	1	D21S11	31	213	354	122
1	1	D21S11	31.2	215	780	285
1	1	D21S11	32.2	219	113	41
1	1	D21S11	33.2	222.897	31	11
1	1	D2S1338	16	310.907	14	7
1	1	D2S1338	17	315	302	155
1	1	D2S1338	18	318.908	23	11
1	1	D2S1338	19	322.903	377	173
1	1	D2S1338	23	338.892	92	36
1	1	D2S1338	24	343	287	135
1	1	D3S1358	8	95.5791	12	6
1	1	D3S1358	13	115.899	39	24
1	1	D3S1358	14	119.896	425	204
1	1	D3S1358	15	124	498	251
1	1	D3S1358	16	127.812	676	293
1	1	D3S1358	17	131.809	46	24
1	1	D3S1358	18	135.81	55	25
1	1	D3S1358	20	144.286	40	20
1	1	D5S818	5.1	127.395	11	6
1	1	D5S818	5.2	128.315	16	6
1	1	D5S818	5.3	129.234	11	5
1	1	D5S818	6.1	130.797	14	6
1	1	D5S818	6.2	132.085	13	7
1	1	D5S818	7	134	43	23
1	1	D5S818	7.1	134.933	10	3
1	1	D5S818	8	137.538	11	4
1	1	D5S818	8.2	140.018	12	6
1	1	D5S818	9	141.822	13	6
1	1	D5S818	9.1	142.798	12	6
1	1	D5S818	9.2	143.945	15	8
1	1	D5S818	10	145.818	93	43
1	1	D5S818	10.2	147.755	17	9
1	1	D5S818	11	149.907	1020	424
1	1	D5S818	11.2	152.22	15	8
1	1	D5S818	12	153.905	365	173
1	1	D5S818	12.2	156.033	10	5
1	1	D5S818	13	158	229	111
1	1	D7S820	8	263	103	47

1	1	D7S820	9	267	176	77
1	1	D7S820	10	271	756	320
1	1	D7S820	11	275	142	67
1	1	D7S820	12	279	568	270
1	1	D8S1179	7.1	120.449	12	6
1	1	D8S1179	7.3	122.325	20	10
1	1	D8S1179	11	135	90	35
1	1	D8S1179	12	139	625	285
1	1	D8S1179	12.2	141.081	14	7
1	1	D8S1179	13	142.911	1306	504
1	1	D8S1179	14	147	635	259
1	1	D8S1179	15	151	433	182
1	1	D8S1179	16.1	155.762	10	3
1	1	FGA	18	221	13	7
1	1	FGA	19	225	204	90
1	1	FGA	20	229	127	51
1	1	FGA	20.2	230.798	14	8
1	1	FGA	21	232.899	481	169
1	1	FGA	21.2	235.155	12	7
1	1	FGA	22	237	144	62
1	1	FGA	23	241	55	29
1	1	FGA	24	245	500	206
1	1	FGA	25	249.299	11	6
1	1	TH01	3.1	159.976	14	6
1	1	TH01	5	167	12	5
1	1	TH01	6	170.901	796	271
1	1	TH01	7	174.9	535	179
1	1	TH01	8	178.898	326	114
1	1	TH01	9	183	299	115
1	1	TH01	9.3	186	192	70
1	1	TPOX	7	225.797	21	9
1	1	TPOX	8	229.791	900	362
1	1	TPOX	10	238	15	7
1	1	TPOX	11	241.899	50	21
1	1	TPOX	12	245.9	119	57
1	1	vWA	9.3	150.261	13	4
1	1	vWA	10.1	151.707	11	3
1	1	vWA	12.1	159.792	13	4
1	1	vWA	13	163	14	6
1	1	vWA	13.1	164.293	12	6
1	1	vWA	13.2	165.117	12	5
1	1	vWA	14	166.902	352	141
1	1	vWA	15	170.897	49	21
1	1	vWA	16	174.901	365	155
1	1	vWA	17	178.898	614	261

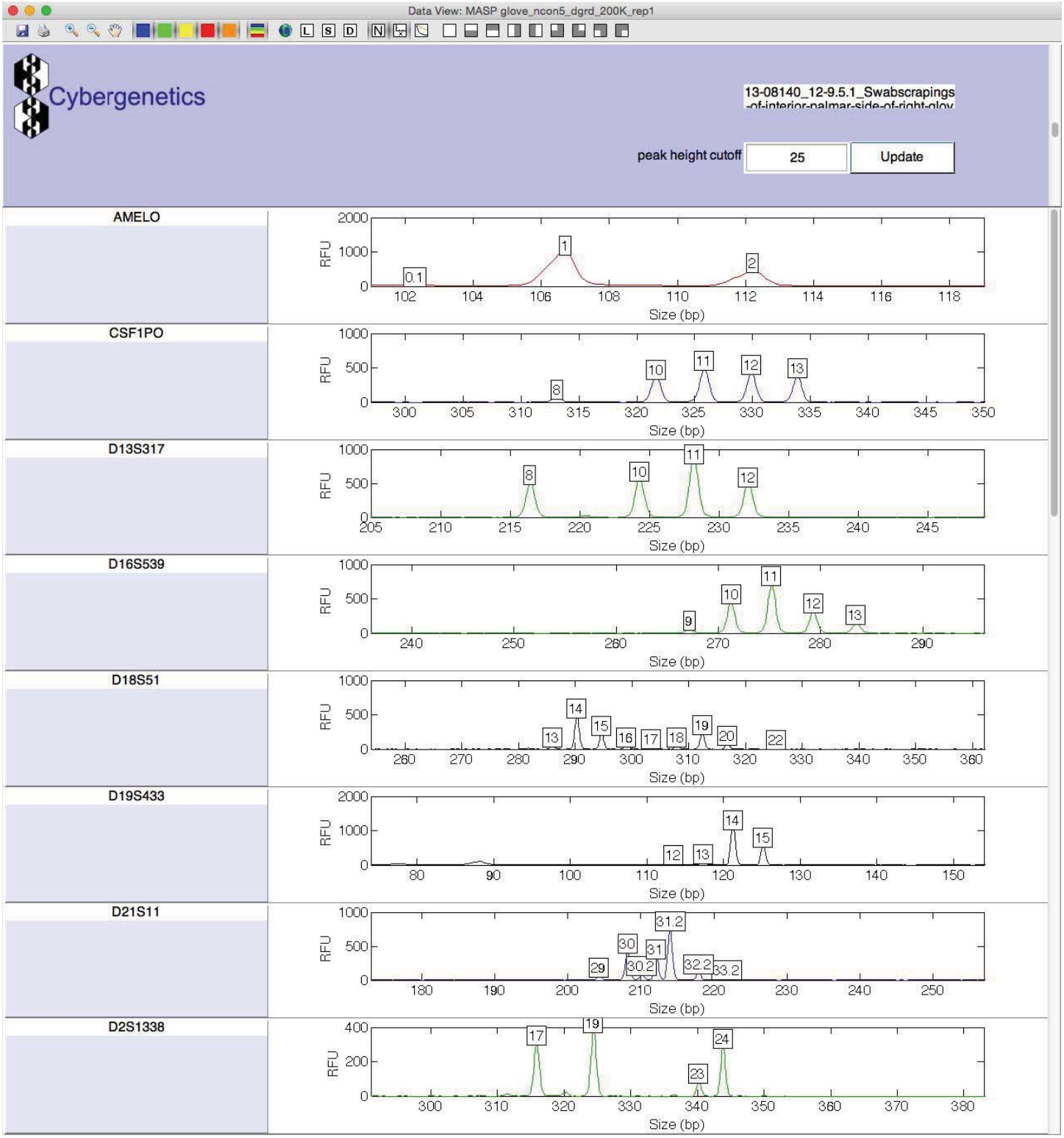
1	1	vWA	18	182.899	357	124
1	1	vWA	19	187	11	3
1	1	vWA	22.1	200.064	13	3

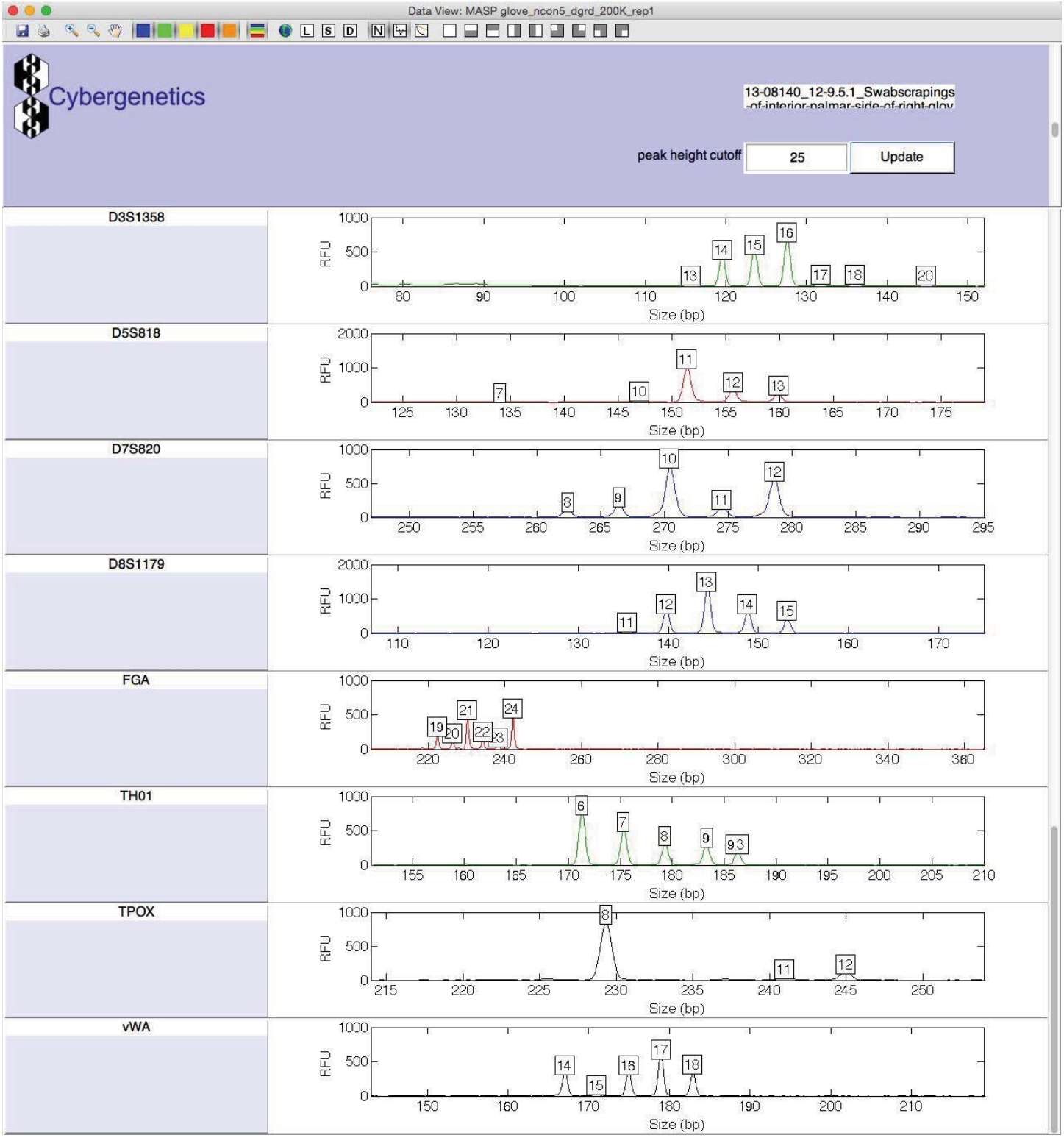
EPG

This section contains the electropherogram (EPG) images as seen in the VUIer™ software. The images show the peaks present for each locus for the Identifiler® kit.

The EPGs are shown in the following order:

Item 12-9.5.1


Data View: MASP glove_ncon5_dgrd_200K_rep1
Cybergenetics
13-08140_12-9.5.1_Swabscrapings
peak height cutoff
25
Update
AMELO
CSF1PO
D13S317
D16S539
D18S51
D19S433
D21S11
D2S1338
RFU
Size (bp)


Data View: MASP glove_ncon5_dgrd_200K_rep1
Cybergenetics
13-08140_12-9.5.1_Swabscrapings
-of-interior-palmar-side-of-right-glov
peak height cutoff
25
Update
D3S1358
D5S818
D7S820
D8S1179
FGA
TH01
TPOX
vWA
RFU
Size (bp)

Lab EPG

This section contains the electropherogram (EPG) images provided by the DNA laboratory. The images show the peaks present for each locus for the Identifiler® kit. Peaks above threshold are labeled.

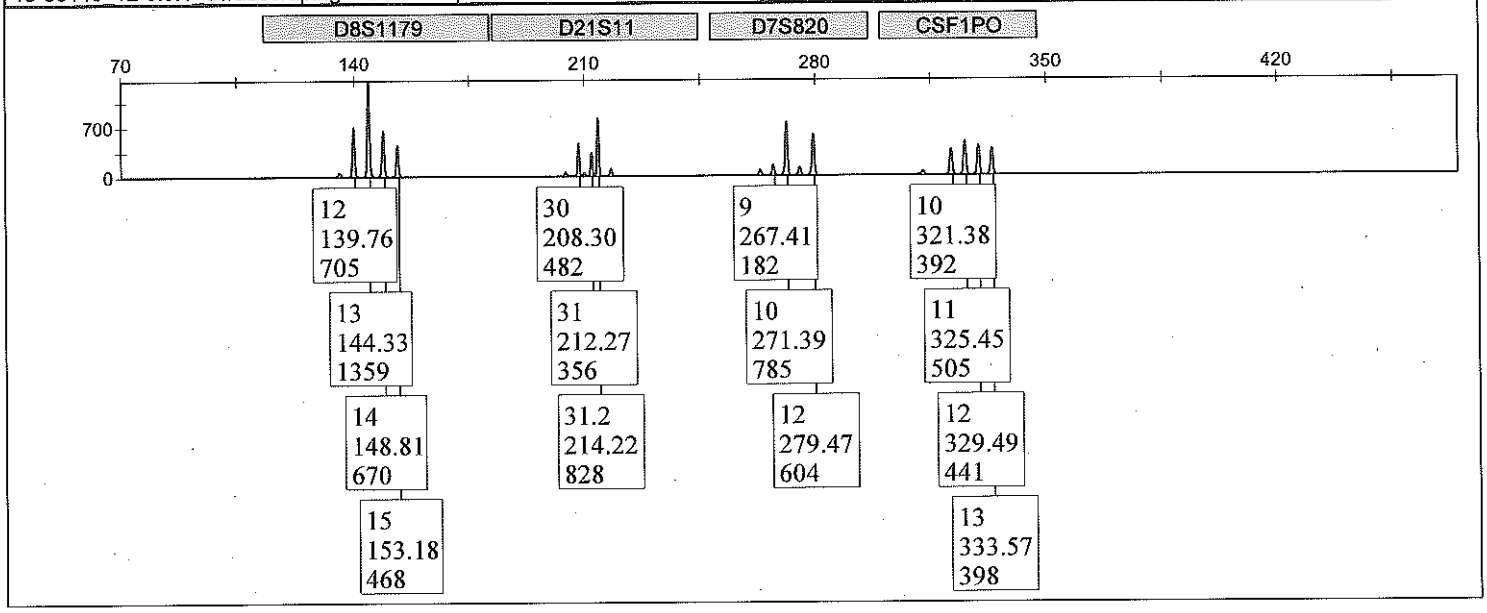
The lab EPGs are shown in the following order:

Item 12-9.5.1

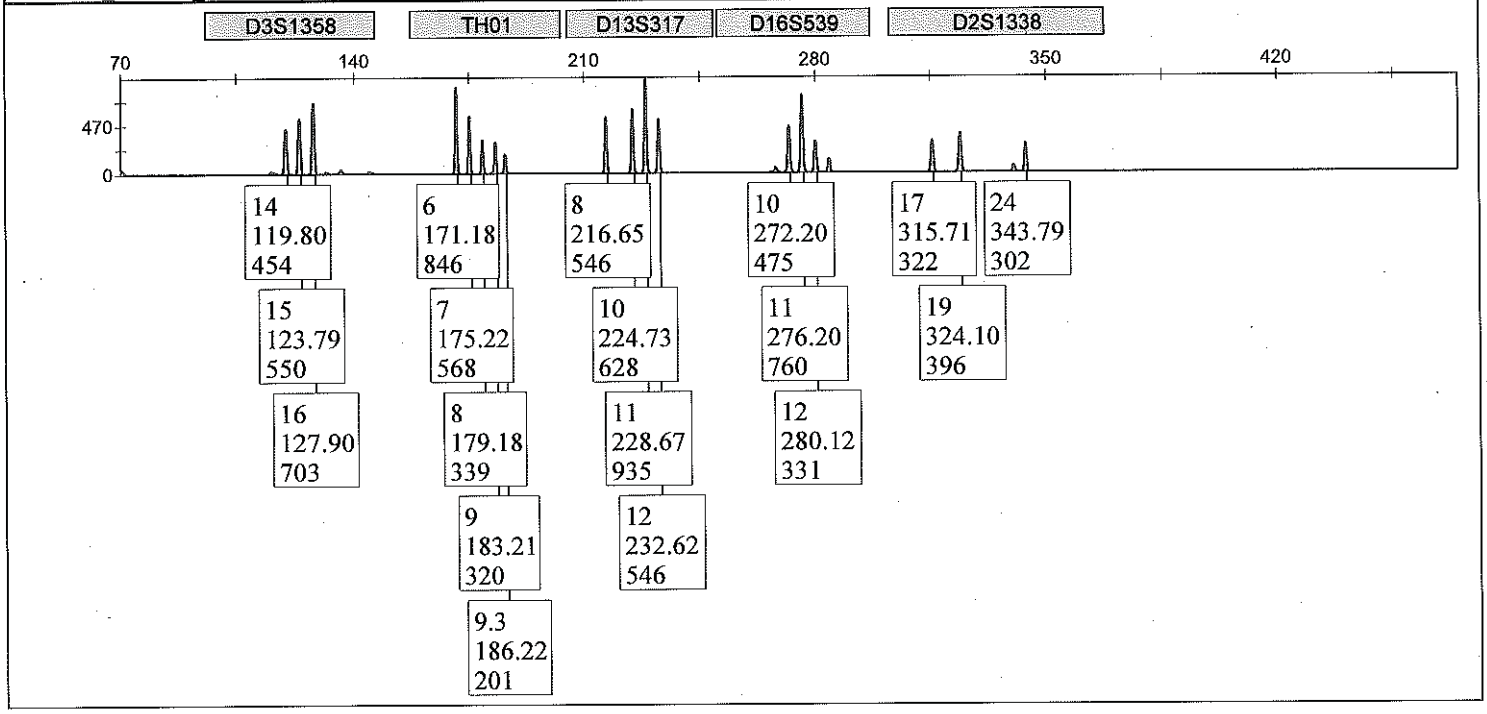
Applied Biosystems
GeneMapper ID v3.2.1

MCE2013-0118A-ID-JSM

Sample Name	Panel	SQO	OS	SQ
13-08140_12-9.5.1_Swabscrapings-of-interior-palmar-side-o…ide-front-floor-area-Honda-Civic-MA-Reg.-116GC7_ID_20-sec	Identifiler_v2			



13-08140_12-9.5.1_Swabscrapings-of-interior-palmar-side-o…ide-front-floor-area-Honda-Civic-MA-Reg.-116GC7_ID_20-sec	Identifiler_v2



13-08140
JM 35

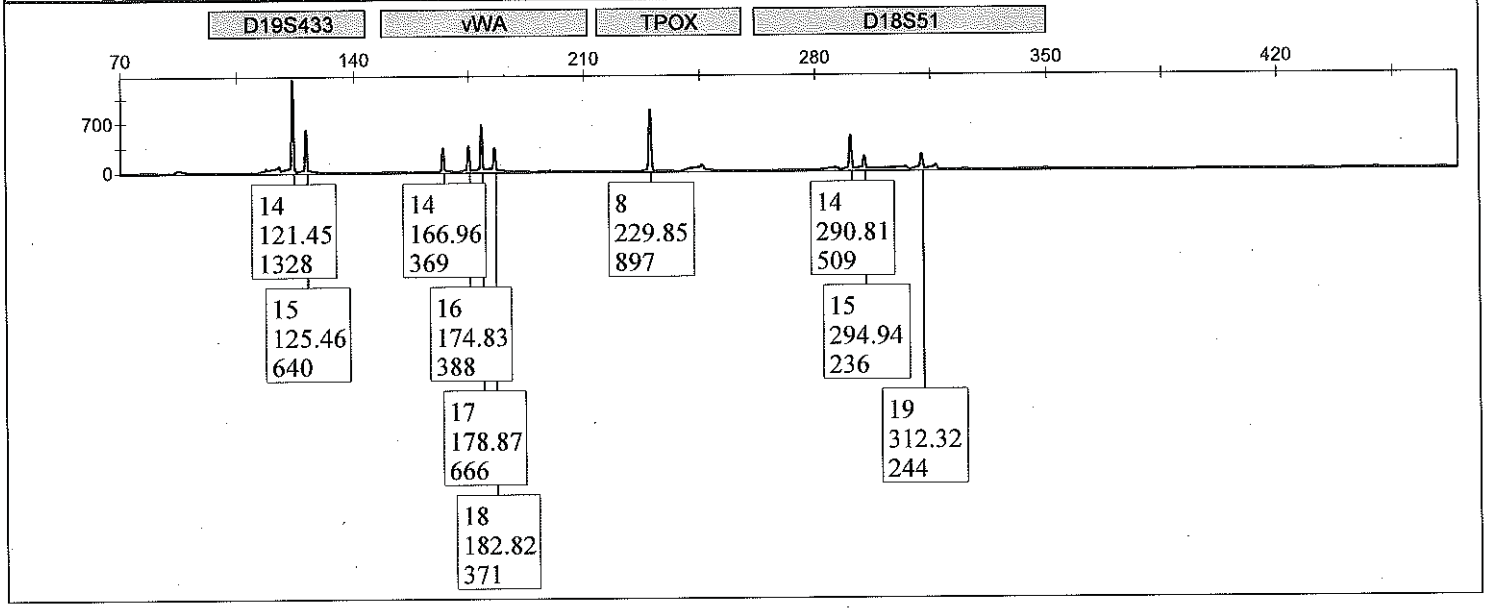
19

Applied Biosystems

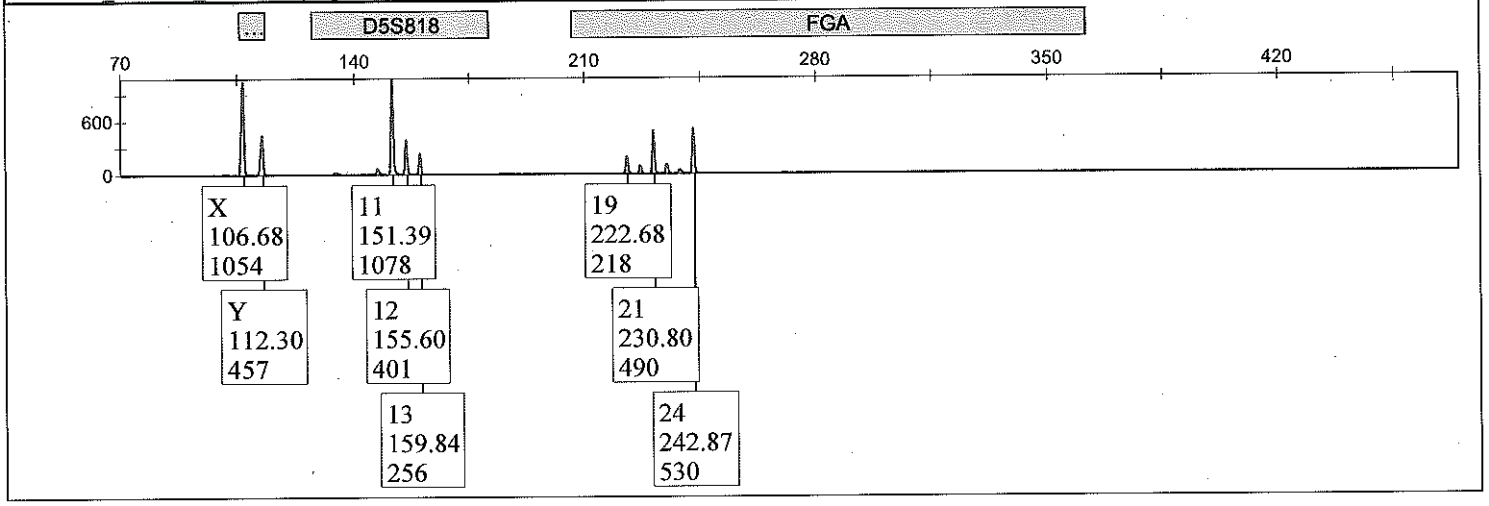
GeneMapper ID v3.2.1

MCE2013-0118A-ID-JSM

Sample Name	Panel	SQO	OS	SQ
13-08140_12-9.5.1_Swabscrapings-of-interior-palmar-side-o…ide-front-floor-area-Honda-Civic-MA-Reg.-116GC7_ID_20-sec	Identifiler_v2			



13-08140_12-9.5.1_Swabscrapings-of-interior-palmar-side-o…ide-front-floor-area-Honda-Civic-MA-Reg.-116GC7_ID_20-sec	Identifiler_v2



13-08140

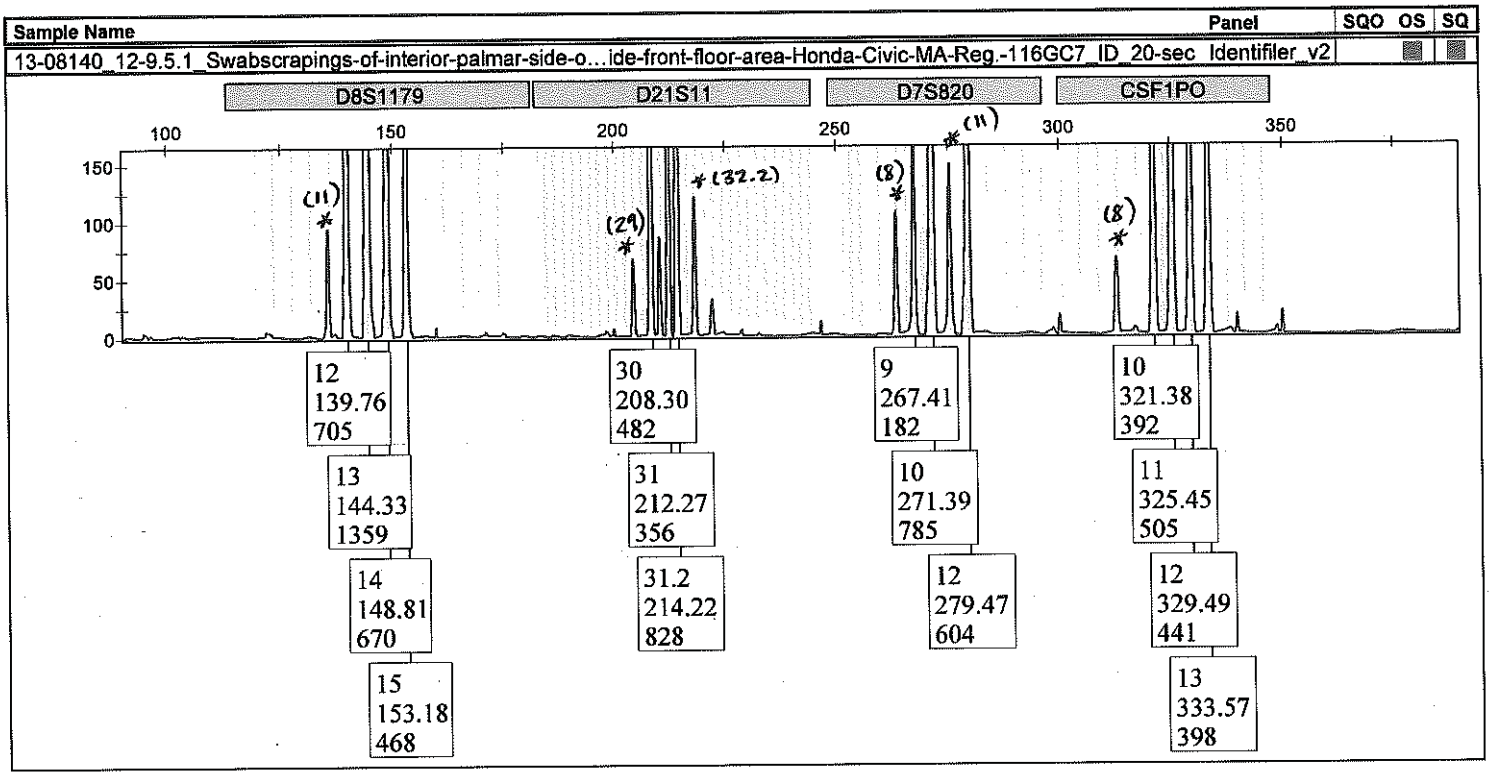
BM36

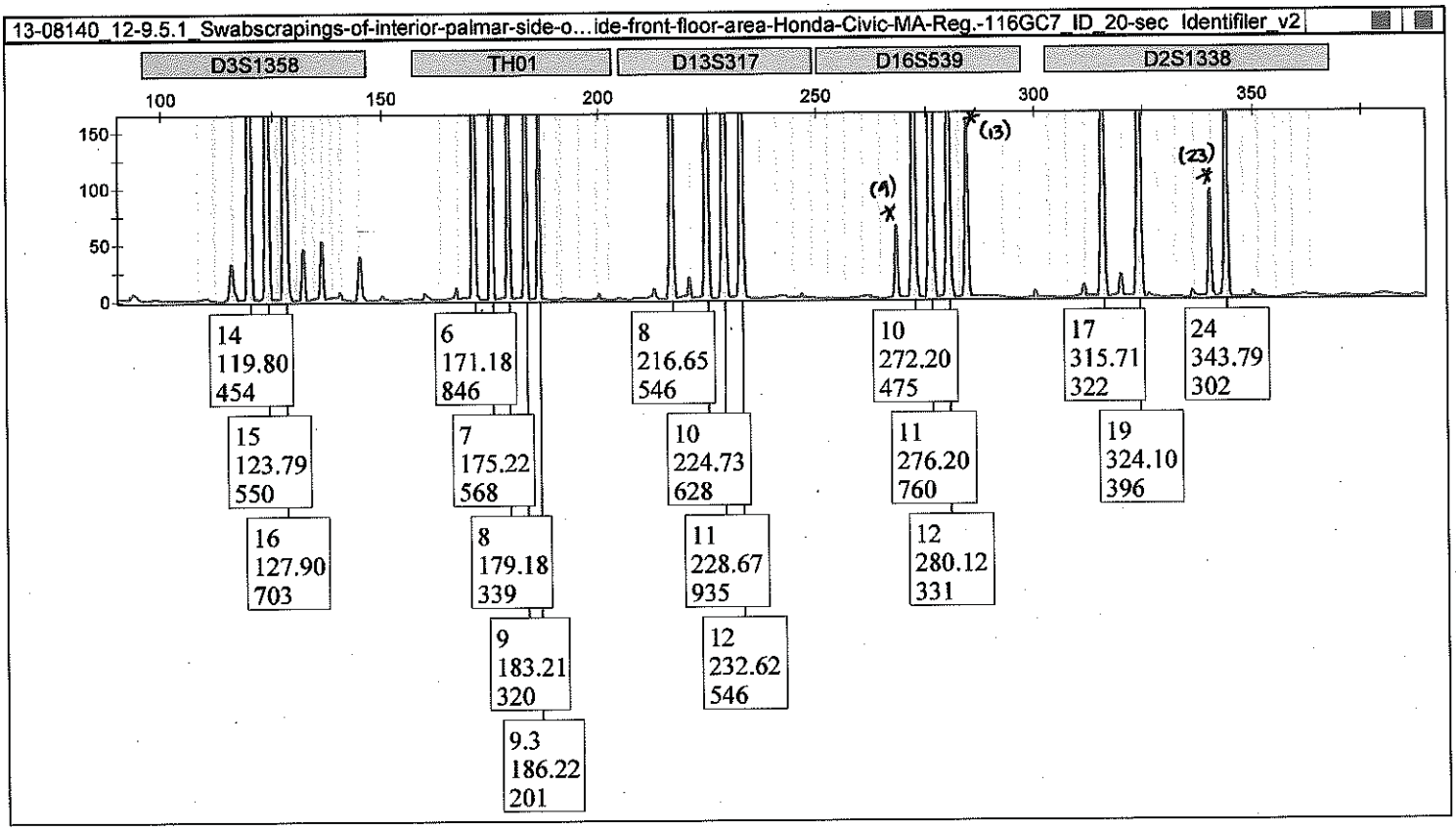
20

Applied Biosystems

GeneMapper ID v3.2.1

MCE2013-0118A-ID-JSM





13-08140

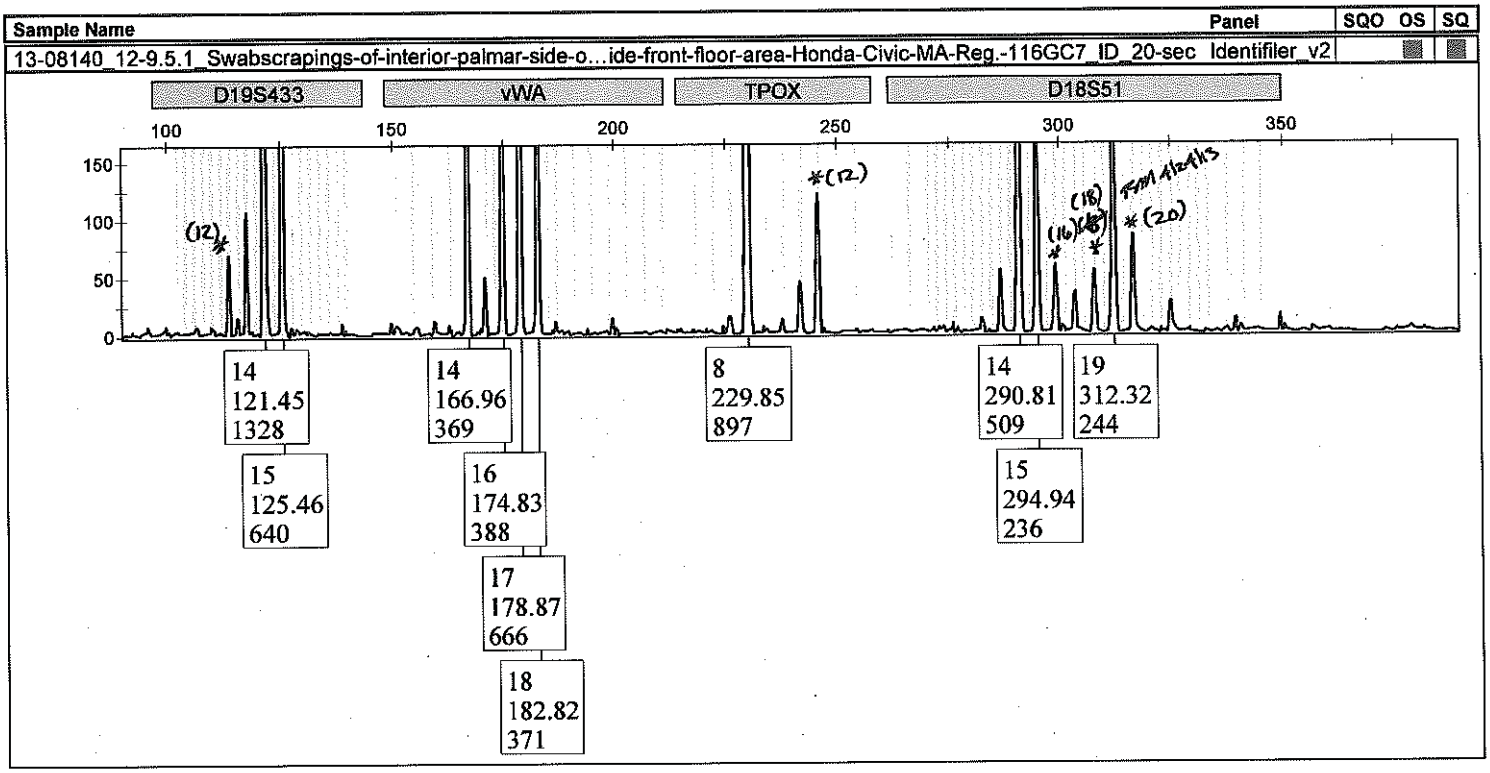
Jom 39

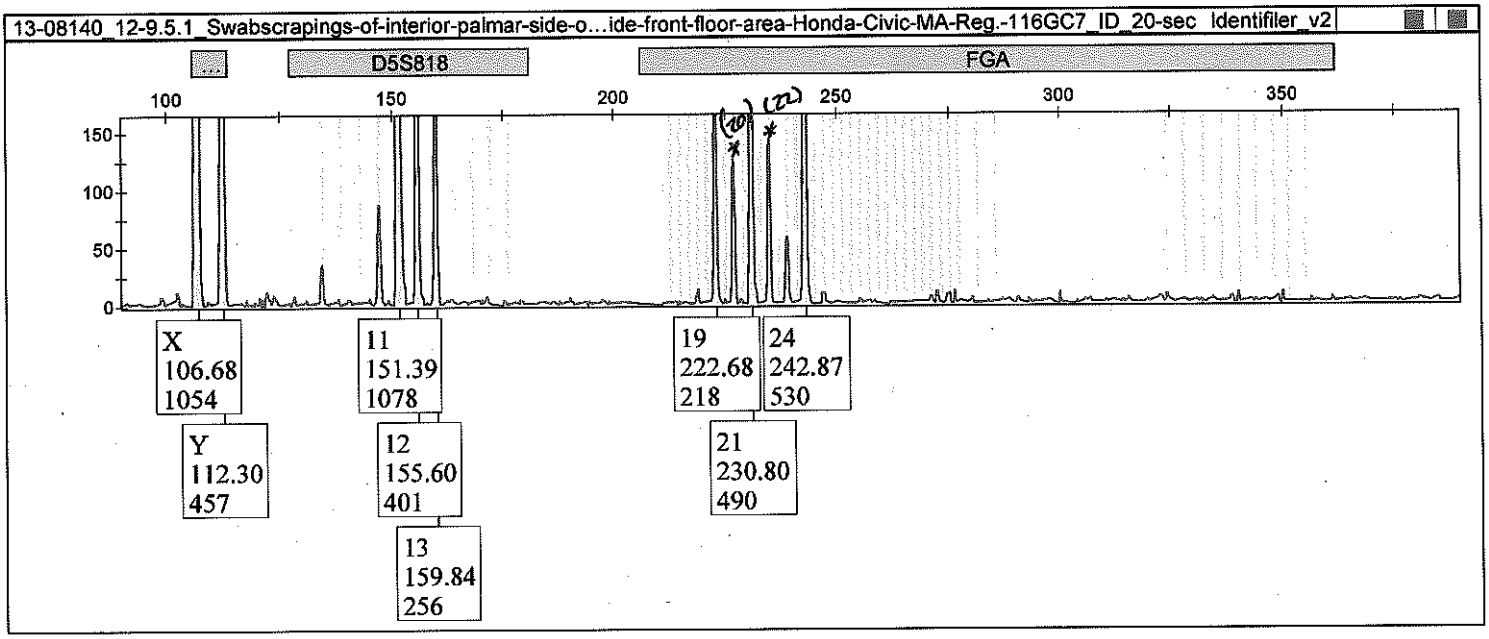
21

Applied Biosystems

GeneMapper ID v3.2.1

MCE2013-0118A-ID-JSM





Form 40

13-08140

22

Request

This section describes the TrueAllele® computer interpretation runs ("requests") that were reviewed on the DNA evidence data in this case, including request run parameters and computer processing times.

Listing

The request table has columns for the name of the computer request, the number of contributors, how many known genotypes were assumed, options that were turned on or off (e.g., degraded), and the number of sampling cycles. The number of cycles is expressed in thousands (e.g., 100K means 100 thousand). The number of burn in cycles is the same as the number of sampling cycles.

Name	Contributors	Known	Degraded DNA	Cycles
glove_ncon3_dgrd_200K	3		on	200K
glove_ncon3_dgrd_200K_rep1	3		on	200K
glove+TT_ncon3_dgrd_200K	3	TT	on	200K
glove+TT_ncon3_dgrd_200K_rep1	3	TT	on	200K
glove_ncon4_dgrd_200K	4		on	200K
glove_ncon4_dgrd_200K_rep1	4		on	200K
glove+TT_ncon4_dgrd_200K	4	TT	on	200K
glove+TT_ncon4_dgrd_200K_rep1	4	TT	on	200K
glove+TT_ncon4_dgrd_200K_rep2	4	TT	on	200K
glove_ncon5_dgrd_200K	5		on	200K
glove_ncon5_dgrd_200K_rep1	5		on	200K
glove_ncon5_dgrd_200K_rep2	5		on	200K
glove+TT_ncon5_dgrd_200K	5	TT	on	200K
glove+TT_ncon5_dgrd_200K_rep1	5	TT	on	200K
glove+TT_ncon5_dgrd_200K_rep2	5	TT	on	200K

Timing

The table shows the computer start and finish dates for each test, and how much time the computer took to process the test (duration).

name	date started	date finished	duration (days, HH:MM)
glove_ncon3_dgrd_200K	Oct 23, 2014	Oct 27, 2014	3 days, 13:52
glove_ncon3_dgrd_200K_rep1	Oct 28, 2014	Nov 1, 2014	3 days, 17:43
glove+TT_ncon3_dgrd_200K	Oct 28, 2014	Oct 31, 2014	2 days, 23:02
glove+TT_ncon3_dgrd_200K_rep1	Oct 28, 2014	Oct 31, 2014	2 days, 21:51
glove_ncon4_dgrd_200K	Oct 23, 2014	Oct 28, 2014	4 days, 19:35
glove_ncon4_dgrd_200K_rep1	Oct 28, 2014	Nov 2, 2014	4 days, 20:02
glove+TT_ncon4_dgrd_200K	Oct 28, 2014	Nov 1, 2014	3 days, 22:18
glove+TT_ncon4_dgrd_200K_rep1	Oct 28, 2014	Nov 1, 2014	4 days, 11:06
glove+TT_ncon4_dgrd_200K_rep2	Nov 5, 2014	Nov 9, 2014	3 days, 23:49
glove_ncon5_dgrd_200K	Nov 5, 2014	Nov 11, 2014	6 days, 01:34
glove_ncon5_dgrd_200K_rep1	Nov 5, 2014	Nov 11, 2014	6 days, 02:47
glove_ncon5_dgrd_200K_rep2	Nov 5, 2014	Nov 11, 2014	6 days, 03:18
glove+TT_ncon5_dgrd_200K	Nov 5, 2014	Nov 10, 2014	5 days, 03:04
glove+TT_ncon5_dgrd_200K_rep1	Nov 5, 2014	Nov 10, 2014	5 days, 02:13
glove+TT_ncon5_dgrd_200K_rep2	Nov 5, 2014	Nov 10, 2014	5 days, 03:52

Genotype

Genotype results are provided for the reported DNA match statistics. When there is uncertainty, allele pair probabilities are given.

Evidence	Computer-inferred contributor genotypes are provided at every locus.
Reference	The reference genotypes used in the case.
Population	The allele frequency data used for population genotypes

Evidence

The genotypes used in the reported DNA match statistics are listed. The genotype tables show the inferred posterior genotype distribution at a confidence level of 99%. The table rows show the probability of one allele pair value (allele1 and allele2) of the inferred contributor genotype, organized by locus.

Item 12-9.5.1 v. suspect 12-1.1.1
glove_ncon5_dgrd_200K_rep1 contributor 2

locus	allele 1	allele 2	probability
AMELO	1	2	0.5740
	1	1	0.4260
CSF1PO	11	13	0.1949
	10	12	0.1485
	11	12	0.1389
	12	13	0.1232
	10	11	0.1225
	10	13	0.1045
	11	11	0.0391
	10	10	0.0289
	8	11	0.0253
	8	10	0.0246
	8	12	0.0168
	12	12	0.0154
	8	13	0.0101
D13S317	10	11	0.1979
	8	11	0.1787
	11	12	0.1579
	10	12	0.1185
	8	10	0.1066
	11	11	0.0931
	8	12	0.0805
	12	12	0.0403
	10	10	0.0078
	9	12	0.0058
	9	11	0.0046
D16S539	10	11	0.3171
	11	12	0.2750
	10	12	0.1163
	11	11	0.0991
	11	13	0.0392
	9	11	0.0309
	12	13	0.0273
	9	13	0.0200
	9	12	0.0198
	10	13	0.0158
	12	12	0.0116
	9	10	0.0096

	9	9	0.0066
	10	10	0.0056
D18S51	14	19	0.2918
	14	15	0.2893
	14	14	0.0979
	15	19	0.0978
	16	20	0.0143
	16	18	0.0137
	15	20	0.0134
	13	16	0.0130
	14	20	0.0125
	13	18	0.0099
	13	20	0.0090
	19	20	0.0085
	15	16	0.0083
	15	15	0.0081
	14	16	0.0081
	13	17	0.0075
	16	17	0.0075
	18	20	0.0075
	17	18	0.0067
	13	14	0.0067
	15	18	0.0066
	15	17	0.0065
	13	15	0.0055
	14	18	0.0050
	17	20	0.0048
	14	17	0.0042
	16	19	0.0033
	19	19	0.0029
	13	19	0.0028
	12	17	0.0027
	17	17	0.0027
	12	16	0.0018
	17	19	0.0018
	12	15	0.0018
	18	18	0.0018
	12	18	0.0014
	18	19	0.0014
	16	16	0.0012
	13	13	0.0011
D19S433	14	15	0.4290

	14	14	0.3533
	15	15	0.0647
	13	14	0.0391
	12	14	0.0291
	12	13	0.0252
	13	15	0.0217
	12	15	0.0206
	13	13	0.0051
	14	15.2	0.0025
D21S11	30	31.2	0.3050
	31	31.2	0.2447
	31.2	31.2	0.1288
	30	31	0.1147
	30	32.2	0.0275
	29	30.2	0.0230
	29	30	0.0181
	31	32.2	0.0178
	31.2	32.2	0.0145
	30	30	0.0121
	30	30.2	0.0115
	29	32.2	0.0109
	30.2	32.2	0.0107
	29	31	0.0104
	29	31.2	0.0094
	29	33.2	0.0065
	30.2	31.2	0.0063
	29	29	0.0044
	31	31	0.0040
	30.2	31	0.0039
	30	33.2	0.0029
	32.2	33.2	0.0023
	30.2	33.2	0.0021
D2S1338	19	24	0.2667
	17	19	0.2499
	17	24	0.1663
	19	19	0.0826
	17	17	0.0515
	17	23	0.0492
	19	23	0.0297
	24	24	0.0214
	23	24	0.0179
	17	18	0.0136

	18	24	0.0090
	18	23	0.0075
	18	19	0.0072
	23	23	0.0070
	17	20	0.0031
	16	18	0.0030
	16	17	0.0023
	16	23	0.0014
	16	24	0.0012
D3S1358	14	16	0.2787
	15	16	0.2383
	14	15	0.1947
	16	16	0.1156
	15	15	0.0438
	17	18	0.0215
	16	18	0.0211
	15	18	0.0191
	16	17	0.0186
	15	17	0.0155
	14	14	0.0131
	14	18	0.0059
	14	17	0.0052
D5S818	11	11	0.3764
	11	12	0.2844
	12	13	0.1051
	11	13	0.0991
	10	11	0.0314
	10	12	0.0272
	12	12	0.0233
	10	13	0.0224
	13	13	0.0085
	7	12	0.0074
	7	11	0.0063
D7S820	10	12	0.4577
	12	12	0.1515
	10	10	0.1107
	9	10	0.0884
	8	11	0.0341
	8	10	0.0333
	10	11	0.0295
	11	12	0.0181
	9	12	0.0167

	8	9	0.0163
	8	12	0.0159
	9	11	0.0104
	8	8	0.0075
D8S1179	13	14	0.2672
	12	13	0.2279
	13	13	0.1036
	14	15	0.0947
	12	14	0.0931
	13	15	0.0841
	12	15	0.0372
	11	13	0.0296
	14	14	0.0142
	11	15	0.0135
	11	14	0.0124
	11	12	0.0088
	12	12	0.0063
FGA	21	24	0.3931
	19	24	0.1627
	19	21	0.1074
	24	24	0.0329
	19	22	0.0323
	19	20	0.0304
	20	22	0.0284
	21	22	0.0242
	21	21	0.0226
	20	24	0.0223
	22	24	0.0218
	20	21	0.0207
	22	23	0.0191
	23	24	0.0181
	20	23	0.0137
	21	23	0.0135
	22	22	0.0090
	20	20	0.0054
	19	23	0.0050
	23	23	0.0031
	24	25	0.0017
	22	25	0.0016
	25	25	0.0015
TH01	6	7	0.3664
	8	9	0.1635

	6	8	0.1163
	6	9	0.0641
	6	6	0.0641
	7	8	0.0498
	7	9	0.0344
	6	9.3	0.0326
	8	9.3	0.0269
	9	9.3	0.0258
	7	9.3	0.0188
	8	8	0.0131
	9	9	0.0086
	9.3	9.3	0.0086
TPOX	8	8	0.7324
	8	12	0.1430
	8	11	0.0619
	8	10	0.0150
	11	12	0.0107
	11	11	0.0095
	10	11	0.0064
	7	8	0.0061
	7	11	0.0034
	12	12	0.0032
vWA	14	17	0.2041
	16	17	0.1673
	17	18	0.1563
	14	18	0.1221
	16	18	0.1035
	14	16	0.0899
	17	17	0.0481
	15	16	0.0203
	15	17	0.0191
	16	16	0.0153
	18	18	0.0139
	15	18	0.0138
	14	15	0.0122
	14	14	0.0100

Item 12-9.5.1 v. suspect 15-1.1
glove_ncon5_dgrd_200K_rep2 contributor 3

locus	allele 1	allele 2	probability
AMELO	1	2	0.5584
	1	1	0.4416
CSF1PO	10	12	0.1689
	11	13	0.1641
	11	12	0.1523
	12	13	0.1291
	10	11	0.1257
	10	13	0.1077
	11	11	0.0511
	12	12	0.0283
	8	11	0.0190
	10	10	0.0141
	8	10	0.0138
	8	12	0.0127
	8	13	0.0042
D13S317	10	11	0.2017
	8	11	0.1582
	8	12	0.1416
	11	12	0.1385
	8	10	0.1064
	10	12	0.1059
	11	11	0.0966
	10	10	0.0159
	12	12	0.0145
	9	11	0.0070
	8	8	0.0056
D16S539	10	11	0.3155
	11	12	0.2901
	11	11	0.1041
	10	12	0.0839
	11	13	0.0551
	10	13	0.0348
	12	13	0.0326
	9	11	0.0191
	9	13	0.0168
	9	12	0.0097
	9	10	0.0084
	13	13	0.0084

	12	12	0.0080
	10	10	0.0070
D18S51	14	15	0.2888
	14	19	0.2797
	14	14	0.1023
	15	19	0.1000
	14	20	0.0225
	16	20	0.0216
	13	18	0.0148
	15	20	0.0139
	13	20	0.0121
	16	18	0.0120
	14	16	0.0095
	15	15	0.0083
	13	16	0.0081
	18	20	0.0078
	13	15	0.0071
	13	17	0.0069
	16	17	0.0067
	13	14	0.0064
	19	20	0.0060
	19	19	0.0057
	17	18	0.0052
	15	18	0.0051
	14	18	0.0049
	14	17	0.0048
	15	16	0.0042
	17	20	0.0040
	15	17	0.0038
	16	19	0.0037
	18	19	0.0031
	12	16	0.0024
	12	17	0.0021
	13	19	0.0015
	17	17	0.0015
	17	19	0.0013
	12	13	0.0013
	12	14	0.0011
D19S433	14	14	0.4213
	14	15	0.3921
	15	15	0.0651
	13	14	0.0379

	13	15	0.0221
	12	13	0.0194
	12	15	0.0148
	12	14	0.0124
	13	13	0.0037
	14	15.2	0.0029
D21S11	30	31.2	0.3178
	31	31.2	0.2477
	30	31	0.1374
	31.2	31.2	0.0914
	30	32.2	0.0316
	30	30	0.0246
	30.2	32.2	0.0191
	31.2	32.2	0.0179
	29	30.2	0.0144
	29	30	0.0141
	30	30.2	0.0127
	29	32.2	0.0121
	31	32.2	0.0087
	29	33.2	0.0074
	29	31	0.0066
	30.2	31.2	0.0055
	29	31.2	0.0052
	29	29	0.0052
	30	33.2	0.0047
	30.2	31	0.0026
	31.2	33.2	0.0023
	31	31	0.0021
D2S1338	19	24	0.2294
	17	19	0.2283
	17	24	0.1543
	19	19	0.1197
	17	17	0.0642
	17	23	0.0524
	23	24	0.0395
	24	24	0.0301
	19	23	0.0275
	18	19	0.0073
	17	18	0.0065
	18	23	0.0064
	23	23	0.0060
	18	24	0.0058

	16	18	0.0034
	16	17	0.0017
	18	18	0.0015
	20	23	0.0013
	18	20	0.0011
	16	23	0.0011
	16	24	0.0010
	20	24	0.0010
	19	20	0.0009
D3S1358	15	16	0.2787
	14	16	0.2524
	14	15	0.1744
	16	16	0.1402
	15	15	0.0529
	14	14	0.0186
	15	18	0.0147
	15	17	0.0126
	17	18	0.0123
	16	17	0.0121
	16	18	0.0098
	14	17	0.0065
	14	18	0.0058
D5S818	11	11	0.4148
	11	12	0.2417
	11	13	0.1274
	12	13	0.1040
	10	11	0.0297
	10	13	0.0183
	12	12	0.0177
	10	12	0.0149
	13	13	0.0144
	7	11	0.0039
	7	13	0.0037
D7S820	10	12	0.4287
	9	10	0.1430
	10	10	0.1062
	12	12	0.1054
	9	11	0.0527
	10	11	0.0322
	9	12	0.0305
	8	10	0.0284
	11	12	0.0177

	8	11	0.0171
	8	9	0.0145
	8	12	0.0074
	9	9	0.0061
D8S1179	13	14	0.2776
	12	13	0.2261
	13	15	0.1190
	14	15	0.0937
	13	13	0.0706
	12	15	0.0563
	12	14	0.0553
	11	13	0.0213
	14	14	0.0205
	15	15	0.0189
	11	14	0.0136
	12	12	0.0114
	11	15	0.0075
FGA	21	24	0.3587
	19	24	0.2066
	19	21	0.0980
	19	22	0.0768
	20	22	0.0321
	21	22	0.0307
	22	24	0.0301
	24	24	0.0235
	20	21	0.0229
	21	21	0.0169
	20	24	0.0164
	20	23	0.0136
	22	23	0.0133
	23	24	0.0125
	19	20	0.0121
	21	23	0.0118
	22	22	0.0044
	19	23	0.0030
	23	26	0.0027
	23	23	0.0024
	20	20	0.0019
TH01	6	7	0.3421
	6	8	0.1446
	8	9	0.1316
	6	9	0.1062

	9	9.3	0.0532
	7	8	0.0468
	6	9.3	0.0332
	7	9	0.0308
	6	6	0.0295
	7	9.3	0.0224
	8	9.3	0.0214
	7	7	0.0123
	9	9	0.0108
	9.3	9.3	0.0073
TPOX	8	8	0.6846
	8	12	0.2132
	8	11	0.0423
	11	12	0.0150
	8	10	0.0093
	10	11	0.0073
	11	11	0.0060
	12	12	0.0052
	7	8	0.0042
	7	11	0.0028
	8	9	0.0025
vWA	14	17	0.1699
	16	17	0.1650
	17	18	0.1426
	16	18	0.1204
	14	16	0.1145
	14	18	0.1050
	17	17	0.0990
	15	17	0.0204
	15	16	0.0142
	16	16	0.0132
	15	18	0.0119
	18	18	0.0077
	14	15	0.0063
	14	14	0.0047

Reference

The reference genotype table shows the allele pair values (allele1 and allele2) for each locus for the reference.

Suspect 12-1.1.1, Dzhokhar Tsarnaev

locus	allele 1	allele 2	probability
AMELO	1	2	1
CSF1PO	11	11	1
D13S317	8	10	1
D16S539	10	12	1
D18S51	14	18	1
D19S433	12	14	1
D21S11	31.2	31.2	1
D2S1338	17	24	1
D3S1358	14	15	1
D5S818	11	12	1
D7S820	10	12	1
D8S1179	13	14	1
FGA	21	24	1
TH01	8	9.3	1
TPOX	8	8	1
vWA	17	18	1

Suspect 15-1.1, Tamerlan A. Tsarnaev

locus	allele 1	allele 2	probability
AMELO	1	2	1
CSF1PO	10	11	1
D13S317	10	11	1
D16S539	10	11	1
D18S51	14	17	1
D19S433	14	15	1
D21S11	30	31.2	1
D2S1338	17	24	1
D3S1358	14	16	1
D5S818	11	13	1
D7S820	10	12	1
D8S1179	13	15	1
FGA	21	24	1
TH01	6	6	1
TPOX	8	12	1
vWA	17	18	1

Population

A population table describes the ethnic sample at each locus, listing for each allele designation the number of counts observed.

United States FBI African American Population

sample	locus	desig	count
US_BLK_FBI	D3S1358	12	1
US_BLK_FBI	D3S1358	13	5
US_BLK_FBI	D3S1358	14	51
US_BLK_FBI	D3S1358	15	122
US_BLK_FBI	D3S1358	15.2	0
US_BLK_FBI	D3S1358	16	129
US_BLK_FBI	D3S1358	17	84
US_BLK_FBI	D3S1358	18	23
US_BLK_FBI	D3S1358	19	2
US_BLK_FBI	vWA	11	1
US_BLK_FBI	vWA	13	2
US_BLK_FBI	vWA	14	24
US_BLK_FBI	vWA	15	85
US_BLK_FBI	vWA	16	97
US_BLK_FBI	vWA	17	66
US_BLK_FBI	vWA	18	49
US_BLK_FBI	vWA	19	26
US_BLK_FBI	vWA	20	10
US_BLK_FBI	vWA	21	0
US_BLK_FBI	FGA	18	3
US_BLK_FBI	FGA	18.2	3
US_BLK_FBI	FGA	19	19
US_BLK_FBI	FGA	19.2	1
US_BLK_FBI	FGA	20	26
US_BLK_FBI	FGA	20.2	0
US_BLK_FBI	FGA	21	45
US_BLK_FBI	FGA	21.2	0
US_BLK_FBI	FGA	22	81
US_BLK_FBI	FGA	22.2	2
US_BLK_FBI	FGA	22.3	0
US_BLK_FBI	FGA	23	45
US_BLK_FBI	FGA	23.2	0
US_BLK_FBI	FGA	24	67
US_BLK_FBI	FGA	24.2	0
US_BLK_FBI	FGA	24.3	0
US_BLK_FBI	FGA	25	36
US_BLK_FBI	FGA	26	13
US_BLK_FBI	FGA	27	8
US_BLK_FBI	FGA	28	6

US_BLK_FBI	FGA	29	2
US_BLK_FBI	FGA	30	1
US_BLK_FBI	D8S1179	9	2
US_BLK_FBI	D8S1179	10	9
US_BLK_FBI	D8S1179	11	13
US_BLK_FBI	D8S1179	12	39
US_BLK_FBI	D8S1179	13	80
US_BLK_FBI	D8S1179	14	120
US_BLK_FBI	D8S1179	15	77
US_BLK_FBI	D8S1179	16	16
US_BLK_FBI	D8S1179	17	3
US_BLK_FBI	D8S1179	18	0
US_BLK_FBI	D21S11	24.2	1
US_BLK_FBI	D21S11	24.3	0
US_BLK_FBI	D21S11	26	1
US_BLK_FBI	D21S11	27	22
US_BLK_FBI	D21S11	28	77
US_BLK_FBI	D21S11	29	68
US_BLK_FBI	D21S11	29.2	1
US_BLK_FBI	D21S11	30	64
US_BLK_FBI	D21S11	30.2	3
US_BLK_FBI	D21S11	30.3	0
US_BLK_FBI	D21S11	31	33
US_BLK_FBI	D21S11	31.2	27
US_BLK_FBI	D21S11	32	3
US_BLK_FBI	D21S11	32.1	0
US_BLK_FBI	D21S11	32.2	25
US_BLK_FBI	D21S11	33	3
US_BLK_FBI	D21S11	33.2	12
US_BLK_FBI	D21S11	34	3
US_BLK_FBI	D21S11	34.2	1
US_BLK_FBI	D21S11	35	10
US_BLK_FBI	D21S11	35.2	0
US_BLK_FBI	D21S11	36	2
US_BLK_FBI	D18S51	11	2
US_BLK_FBI	D18S51	12	21
US_BLK_FBI	D18S51	13	20
US_BLK_FBI	D18S51	13.2	2
US_BLK_FBI	D18S51	14	23
US_BLK_FBI	D18S51	14.2	0
US_BLK_FBI	D18S51	15	60
US_BLK_FBI	D18S51	15.2	0

US_BLK_FBI	D18S51	16	68
US_BLK_FBI	D18S51	17	59
US_BLK_FBI	D18S51	18	47
US_BLK_FBI	D18S51	19	28
US_BLK_FBI	D18S51	20	20
US_BLK_FBI	D18S51	21	4
US_BLK_FBI	D18S51	21.2	0
US_BLK_FBI	D18S51	22	2
US_BLK_FBI	D5S818	7	1
US_BLK_FBI	D5S818	8	18
US_BLK_FBI	D5S818	9	5
US_BLK_FBI	D5S818	10	23
US_BLK_FBI	D5S818	11	94
US_BLK_FBI	D5S818	12	128
US_BLK_FBI	D5S818	13	88
US_BLK_FBI	D5S818	14	2
US_BLK_FBI	D5S818	15	0
US_BLK_FBI	D13S317	7	0
US_BLK_FBI	D13S317	8	13
US_BLK_FBI	D13S317	9	10
US_BLK_FBI	D13S317	10	18
US_BLK_FBI	D13S317	11	85
US_BLK_FBI	D13S317	12	173
US_BLK_FBI	D13S317	13	45
US_BLK_FBI	D13S317	14	13
US_BLK_FBI	D13S317	15	1
US_BLK_FBI	D7S820	6	0
US_BLK_FBI	D7S820	7	3
US_BLK_FBI	D7S820	8	73
US_BLK_FBI	D7S820	9	66
US_BLK_FBI	D7S820	10	136
US_BLK_FBI	D7S820	10.1	0
US_BLK_FBI	D7S820	11	94
US_BLK_FBI	D7S820	11.3	0
US_BLK_FBI	D7S820	12	38
US_BLK_FBI	D7S820	13	8
US_BLK_FBI	D7S820	14	2
US_BLK_FBI	CSF1PO	6	0
US_BLK_FBI	CSF1PO	7	18
US_BLK_FBI	CSF1PO	8	36
US_BLK_FBI	CSF1PO	9	14
US_BLK_FBI	CSF1PO	10	114

US_BLK_FBI	CSF1PO	10.3	0
US_BLK_FBI	CSF1PO	11	86
US_BLK_FBI	CSF1PO	12	126
US_BLK_FBI	CSF1PO	13	23
US_BLK_FBI	CSF1PO	14	3
US_BLK_FBI	CSF1PO	15	0
US_BLK_FBI	TPOX	6	36
US_BLK_FBI	TPOX	7	9
US_BLK_FBI	TPOX	8	154
US_BLK_FBI	TPOX	9	76
US_BLK_FBI	TPOX	10	39
US_BLK_FBI	TPOX	11	94
US_BLK_FBI	TPOX	12	10
US_BLK_FBI	TPOX	13	0
US_BLK_FBI	TH01	5	0
US_BLK_FBI	TH01	6	46
US_BLK_FBI	TH01	7	185
US_BLK_FBI	TH01	8	78
US_BLK_FBI	TH01	8.3	0
US_BLK_FBI	TH01	9	61
US_BLK_FBI	TH01	9.3	44
US_BLK_FBI	TH01	10	6
US_BLK_FBI	D16S539	8	15
US_BLK_FBI	D16S539	9	83
US_BLK_FBI	D16S539	10	46
US_BLK_FBI	D16S539	11	123
US_BLK_FBI	D16S539	12	78
US_BLK_FBI	D16S539	13	69
US_BLK_FBI	D16S539	14	4
US_BLK_FBI	D16S539	15	0
US_BLK_FBI	D2S1338	16	15
US_BLK_FBI	D2S1338	17	34
US_BLK_FBI	D2S1338	18	22
US_BLK_FBI	D2S1338	19	46
US_BLK_FBI	D2S1338	20	21
US_BLK_FBI	D2S1338	21	51
US_BLK_FBI	D2S1338	22	46
US_BLK_FBI	D2S1338	23	33
US_BLK_FBI	D2S1338	24	31
US_BLK_FBI	D2S1338	25	28
US_BLK_FBI	D2S1338	26	7
US_BLK_FBI	D2S1338	27	0

US_BLK_FBI	D19S433	9	0
US_BLK_FBI	D19S433	10	5
US_BLK_FBI	D19S433	11	23
US_BLK_FBI	D19S433	12	38
US_BLK_FBI	D19S433	12.2	27
US_BLK_FBI	D19S433	13	99
US_BLK_FBI	D19S433	13.2	17
US_BLK_FBI	D19S433	14	66
US_BLK_FBI	D19S433	14.2	18
US_BLK_FBI	D19S433	15	13
US_BLK_FBI	D19S433	15.2	13
US_BLK_FBI	D19S433	16	7
US_BLK_FBI	D19S433	16.2	6
US_BLK_FBI	D19S433	17.2	1
US_BLK_FBI	D19S433	18.2	1

United States FBI Caucasian Population

sample	locus	desig	count
US_CAU_FBI	D3S1358	12	0
US_CAU_FBI	D3S1358	13	1
US_CAU_FBI	D3S1358	14	57
US_CAU_FBI	D3S1358	15	100
US_CAU_FBI	D3S1358	15.2	0
US_CAU_FBI	D3S1358	16	94
US_CAU_FBI	D3S1358	17	86
US_CAU_FBI	D3S1358	18	66
US_CAU_FBI	D3S1358	19	2
US_CAU_FBI	vWA	11	0
US_CAU_FBI	vWA	13	2
US_CAU_FBI	vWA	14	40
US_CAU_FBI	vWA	15	44
US_CAU_FBI	vWA	16	79
US_CAU_FBI	vWA	17	103
US_CAU_FBI	vWA	18	87
US_CAU_FBI	vWA	19	33
US_CAU_FBI	vWA	20	4
US_CAU_FBI	vWA	21	0
US_CAU_FBI	FGA	18	12
US_CAU_FBI	FGA	18.2	0
US_CAU_FBI	FGA	19	22
US_CAU_FBI	FGA	19.2	0
US_CAU_FBI	FGA	20	57
US_CAU_FBI	FGA	20.2	1
US_CAU_FBI	FGA	21	68
US_CAU_FBI	FGA	21.2	0
US_CAU_FBI	FGA	22	74
US_CAU_FBI	FGA	22.2	4
US_CAU_FBI	FGA	22.3	0
US_CAU_FBI	FGA	23	62
US_CAU_FBI	FGA	23.2	0
US_CAU_FBI	FGA	24	54
US_CAU_FBI	FGA	24.2	0
US_CAU_FBI	FGA	24.3	0
US_CAU_FBI	FGA	25	27
US_CAU_FBI	FGA	26	7
US_CAU_FBI	FGA	27	4
US_CAU_FBI	FGA	28	0

US_CAU_FBI	FGA	29	0
US_CAU_FBI	FGA	30	0
US_CAU_FBI	D8S1179	9	4
US_CAU_FBI	D8S1179	10	40
US_CAU_FBI	D8S1179	11	23
US_CAU_FBI	D8S1179	12	57
US_CAU_FBI	D8S1179	13	133
US_CAU_FBI	D8S1179	14	79
US_CAU_FBI	D8S1179	15	43
US_CAU_FBI	D8S1179	16	5
US_CAU_FBI	D8S1179	17	1
US_CAU_FBI	D8S1179	18	0
US_CAU_FBI	D21S11	24.2	2
US_CAU_FBI	D21S11	24.3	0
US_CAU_FBI	D21S11	26	0
US_CAU_FBI	D21S11	27	18
US_CAU_FBI	D21S11	28	65
US_CAU_FBI	D21S11	29	71
US_CAU_FBI	D21S11	29.2	0
US_CAU_FBI	D21S11	30	91
US_CAU_FBI	D21S11	30.2	15
US_CAU_FBI	D21S11	30.3	0
US_CAU_FBI	D21S11	31	28
US_CAU_FBI	D21S11	31.2	39
US_CAU_FBI	D21S11	32	6
US_CAU_FBI	D21S11	32.1	0
US_CAU_FBI	D21S11	32.2	44
US_CAU_FBI	D21S11	33	0
US_CAU_FBI	D21S11	33.2	12
US_CAU_FBI	D21S11	34	0
US_CAU_FBI	D21S11	34.2	0
US_CAU_FBI	D21S11	35	0
US_CAU_FBI	D21S11	35.2	1
US_CAU_FBI	D21S11	36	0
US_CAU_FBI	D18S51	11	5
US_CAU_FBI	D18S51	12	50
US_CAU_FBI	D18S51	13	48
US_CAU_FBI	D18S51	13.2	0
US_CAU_FBI	D18S51	14	68
US_CAU_FBI	D18S51	14.2	0
US_CAU_FBI	D18S51	15	50
US_CAU_FBI	D18S51	15.2	0

US_CAU_FBI	D18S51	16	42
US_CAU_FBI	D18S51	17	61
US_CAU_FBI	D18S51	18	36
US_CAU_FBI	D18S51	19	14
US_CAU_FBI	D18S51	20	10
US_CAU_FBI	D18S51	21	2
US_CAU_FBI	D18S51	21.2	0
US_CAU_FBI	D18S51	22	1
US_CAU_FBI	D5S818	7	0
US_CAU_FBI	D5S818	8	0
US_CAU_FBI	D5S818	9	12
US_CAU_FBI	D5S818	10	19
US_CAU_FBI	D5S818	11	160
US_CAU_FBI	D5S818	12	138
US_CAU_FBI	D5S818	13	57
US_CAU_FBI	D5S818	14	3
US_CAU_FBI	D5S818	15	1
US_CAU_FBI	D13S317	7	0
US_CAU_FBI	D13S317	8	39
US_CAU_FBI	D13S317	9	30
US_CAU_FBI	D13S317	10	20
US_CAU_FBI	D13S317	11	125
US_CAU_FBI	D13S317	12	121
US_CAU_FBI	D13S317	13	43
US_CAU_FBI	D13S317	14	14
US_CAU_FBI	D13S317	15	0
US_CAU_FBI	D7S820	6	1
US_CAU_FBI	D7S820	7	7
US_CAU_FBI	D7S820	8	66
US_CAU_FBI	D7S820	9	60
US_CAU_FBI	D7S820	10	118
US_CAU_FBI	D7S820	10.1	0
US_CAU_FBI	D7S820	11	82
US_CAU_FBI	D7S820	11.3	0
US_CAU_FBI	D7S820	12	57
US_CAU_FBI	D7S820	13	12
US_CAU_FBI	D7S820	14	3
US_CAU_FBI	CSF1PO	6	0
US_CAU_FBI	CSF1PO	7	1
US_CAU_FBI	CSF1PO	8	2
US_CAU_FBI	CSF1PO	9	8
US_CAU_FBI	CSF1PO	10	103

US_CAU_FBI	CSF1PO	10.3	1
US_CAU_FBI	CSF1PO	11	122
US_CAU_FBI	CSF1PO	12	132
US_CAU_FBI	CSF1PO	13	29
US_CAU_FBI	CSF1PO	14	6
US_CAU_FBI	CSF1PO	15	2
US_CAU_FBI	TPOX	6	0
US_CAU_FBI	TPOX	7	1
US_CAU_FBI	TPOX	8	221
US_CAU_FBI	TPOX	9	50
US_CAU_FBI	TPOX	10	15
US_CAU_FBI	TPOX	11	103
US_CAU_FBI	TPOX	12	16
US_CAU_FBI	TPOX	13	0
US_CAU_FBI	TH01	5	0
US_CAU_FBI	TH01	6	92
US_CAU_FBI	TH01	7	70
US_CAU_FBI	TH01	8	51
US_CAU_FBI	TH01	8.3	1
US_CAU_FBI	TH01	9	67
US_CAU_FBI	TH01	9.3	124
US_CAU_FBI	TH01	10	1
US_CAU_FBI	D16S539	8	8
US_CAU_FBI	D16S539	9	42
US_CAU_FBI	D16S539	10	27
US_CAU_FBI	D16S539	11	110
US_CAU_FBI	D16S539	12	137
US_CAU_FBI	D16S539	13	66
US_CAU_FBI	D16S539	14	13
US_CAU_FBI	D16S539	15	1
US_CAU_FBI	D2S1338	16	9
US_CAU_FBI	D2S1338	17	59
US_CAU_FBI	D2S1338	18	16
US_CAU_FBI	D2S1338	19	44
US_CAU_FBI	D2S1338	20	47
US_CAU_FBI	D2S1338	21	6
US_CAU_FBI	D2S1338	22	9
US_CAU_FBI	D2S1338	23	41
US_CAU_FBI	D2S1338	24	37
US_CAU_FBI	D2S1338	25	29
US_CAU_FBI	D2S1338	26	7
US_CAU_FBI	D2S1338	27	0

US_CAU_FBI	D19S433	9	0
US_CAU_FBI	D19S433	10	0
US_CAU_FBI	D19S433	11	0
US_CAU_FBI	D19S433	12	33
US_CAU_FBI	D19S433	12.2	2
US_CAU_FBI	D19S433	13	86
US_CAU_FBI	D19S433	13.2	8
US_CAU_FBI	D19S433	14	102
US_CAU_FBI	D19S433	14.2	1
US_CAU_FBI	D19S433	15	41
US_CAU_FBI	D19S433	15.2	8
US_CAU_FBI	D19S433	16	13
US_CAU_FBI	D19S433	16.2	8
US_CAU_FBI	D19S433	17.2	1
US_CAU_FBI	D19S433	18.2	1

United States FBI Hispanic Population

sample	locus	desig	count
US_HIS_FBI	D3S1358	12	0
US_HIS_FBI	D3S1358	13	1
US_HIS_FBI	D3S1358	14	33
US_HIS_FBI	D3S1358	15	178
US_HIS_FBI	D3S1358	15.2	0
US_HIS_FBI	D3S1358	16	111
US_HIS_FBI	D3S1358	17	53
US_HIS_FBI	D3S1358	18	35
US_HIS_FBI	D3S1358	19	6
US_HIS_FBI	vWA	11	1
US_HIS_FBI	vWA	13	0
US_HIS_FBI	vWA	14	25
US_HIS_FBI	vWA	15	31
US_HIS_FBI	vWA	16	146
US_HIS_FBI	vWA	17	90
US_HIS_FBI	vWA	18	79
US_HIS_FBI	vWA	19	29
US_HIS_FBI	vWA	20	5
US_HIS_FBI	vWA	21	0
US_HIS_FBI	FGA	18	1
US_HIS_FBI	FGA	18.2	0
US_HIS_FBI	FGA	19	32
US_HIS_FBI	FGA	19.2	0
US_HIS_FBI	FGA	20	29
US_HIS_FBI	FGA	20.2	1
US_HIS_FBI	FGA	21	53
US_HIS_FBI	FGA	21.2	1
US_HIS_FBI	FGA	22	72
US_HIS_FBI	FGA	22.2	2
US_HIS_FBI	FGA	22.3	0
US_HIS_FBI	FGA	23	57
US_HIS_FBI	FGA	23.2	3
US_HIS_FBI	FGA	24	51
US_HIS_FBI	FGA	24.2	0
US_HIS_FBI	FGA	24.3	0
US_HIS_FBI	FGA	25	56
US_HIS_FBI	FGA	26	34
US_HIS_FBI	FGA	27	13
US_HIS_FBI	FGA	28	1

US_HIS_FBI	FGA	29	0
US_HIS_FBI	FGA	30	0
US_HIS_FBI	D8S1179	9	1
US_HIS_FBI	D8S1179	10	38
US_HIS_FBI	D8S1179	11	25
US_HIS_FBI	D8S1179	12	49
US_HIS_FBI	D8S1179	13	132
US_HIS_FBI	D8S1179	14	100
US_HIS_FBI	D8S1179	15	47
US_HIS_FBI	D8S1179	16	10
US_HIS_FBI	D8S1179	17	3
US_HIS_FBI	D8S1179	18	0
US_HIS_FBI	D21S11	24.2	1
US_HIS_FBI	D21S11	24.3	0
US_HIS_FBI	D21S11	26	0
US_HIS_FBI	D21S11	27	4
US_HIS_FBI	D21S11	28	28
US_HIS_FBI	D21S11	29	83
US_HIS_FBI	D21S11	29.2	1
US_HIS_FBI	D21S11	30	134
US_HIS_FBI	D21S11	30.2	13
US_HIS_FBI	D21S11	30.3	0
US_HIS_FBI	D21S11	31	28
US_HIS_FBI	D21S11	31.2	35
US_HIS_FBI	D21S11	32	5
US_HIS_FBI	D21S11	32.1	0
US_HIS_FBI	D21S11	32.2	55
US_HIS_FBI	D21S11	33	0
US_HIS_FBI	D21S11	33.2	17
US_HIS_FBI	D21S11	34	0
US_HIS_FBI	D21S11	34.2	2
US_HIS_FBI	D21S11	35	0
US_HIS_FBI	D21S11	35.2	0
US_HIS_FBI	D21S11	36	0
US_HIS_FBI	D18S51	11	5
US_HIS_FBI	D18S51	12	43
US_HIS_FBI	D18S51	13	69
US_HIS_FBI	D18S51	13.2	0
US_HIS_FBI	D18S51	14	69
US_HIS_FBI	D18S51	14.2	0
US_HIS_FBI	D18S51	15	56
US_HIS_FBI	D18S51	15.2	0

US_HIS_FBI	D18S51	16	47
US_HIS_FBI	D18S51	17	56
US_HIS_FBI	D18S51	18	21
US_HIS_FBI	D18S51	19	15
US_HIS_FBI	D18S51	20	7
US_HIS_FBI	D18S51	21	8
US_HIS_FBI	D18S51	21.2	0
US_HIS_FBI	D18S51	22	3
US_HIS_FBI	D5S818	7	25
US_HIS_FBI	D5S818	8	1
US_HIS_FBI	D5S818	9	22
US_HIS_FBI	D5S818	10	27
US_HIS_FBI	D5S818	11	171
US_HIS_FBI	D5S818	12	118
US_HIS_FBI	D5S818	13	39
US_HIS_FBI	D5S818	14	2
US_HIS_FBI	D5S818	15	1
US_HIS_FBI	D13S317	7	0
US_HIS_FBI	D13S317	8	27
US_HIS_FBI	D13S317	9	89
US_HIS_FBI	D13S317	10	41
US_HIS_FBI	D13S317	11	82
US_HIS_FBI	D13S317	12	88
US_HIS_FBI	D13S317	13	56
US_HIS_FBI	D13S317	14	23
US_HIS_FBI	D13S317	15	0
US_HIS_FBI	D7S820	6	1
US_HIS_FBI	D7S820	7	9
US_HIS_FBI	D7S820	8	41
US_HIS_FBI	D7S820	9	20
US_HIS_FBI	D7S820	10	128
US_HIS_FBI	D7S820	10.1	0
US_HIS_FBI	D7S820	11	121
US_HIS_FBI	D7S820	11.3	0
US_HIS_FBI	D7S820	12	80
US_HIS_FBI	D7S820	13	16
US_HIS_FBI	D7S820	14	2
US_HIS_FBI	CSF1PO	6	0
US_HIS_FBI	CSF1PO	7	1
US_HIS_FBI	CSF1PO	8	0
US_HIS_FBI	CSF1PO	9	3
US_HIS_FBI	CSF1PO	10	106

US_HIS_FBI	CSF1PO	10.3	0
US_HIS_FBI	CSF1PO	11	111
US_HIS_FBI	CSF1PO	12	164
US_HIS_FBI	CSF1PO	13	27
US_HIS_FBI	CSF1PO	14	4
US_HIS_FBI	CSF1PO	15	2
US_HIS_FBI	TPOX	6	2
US_HIS_FBI	TPOX	7	2
US_HIS_FBI	TPOX	8	232
US_HIS_FBI	TPOX	9	14
US_HIS_FBI	TPOX	10	14
US_HIS_FBI	TPOX	11	114
US_HIS_FBI	TPOX	12	39
US_HIS_FBI	TPOX	13	1
US_HIS_FBI	TH01	5	1
US_HIS_FBI	TH01	6	97
US_HIS_FBI	TH01	7	141
US_HIS_FBI	TH01	8	34
US_HIS_FBI	TH01	8.3	0
US_HIS_FBI	TH01	9	43
US_HIS_FBI	TH01	9.3	101
US_HIS_FBI	TH01	10	1
US_HIS_FBI	D16S539	8	7
US_HIS_FBI	D16S539	9	33
US_HIS_FBI	D16S539	10	72
US_HIS_FBI	D16S539	11	131
US_HIS_FBI	D16S539	12	119
US_HIS_FBI	D16S539	13	43
US_HIS_FBI	D16S539	14	10
US_HIS_FBI	D16S539	15	1
US_HIS_FBI	D2S1338	16	5
US_HIS_FBI	D2S1338	17	63
US_HIS_FBI	D2S1338	18	12
US_HIS_FBI	D2S1338	19	74
US_HIS_FBI	D2S1338	20	40
US_HIS_FBI	D2S1338	21	3
US_HIS_FBI	D2S1338	22	20
US_HIS_FBI	D2S1338	23	35
US_HIS_FBI	D2S1338	24	19
US_HIS_FBI	D2S1338	25	11
US_HIS_FBI	D2S1338	26	2
US_HIS_FBI	D2S1338	27	0

US_HIS_FBI	D19S433	9	1
US_HIS_FBI	D19S433	10	0
US_HIS_FBI	D19S433	11	1
US_HIS_FBI	D19S433	12	16
US_HIS_FBI	D19S433	12.2	6
US_HIS_FBI	D19S433	13	46
US_HIS_FBI	D19S433	13.2	31
US_HIS_FBI	D19S433	14	91
US_HIS_FBI	D19S433	14.2	13
US_HIS_FBI	D19S433	15	34
US_HIS_FBI	D19S433	15.2	23
US_HIS_FBI	D19S433	16	12
US_HIS_FBI	D19S433	16.2	10
US_HIS_FBI	D19S433	17.2	0
US_HIS_FBI	D19S433	18.2	0

Match

DNA match statistic (likelihood ratio) results are reported for genotype comparisons between evidence and reference relative to a population. Each match table appears twice, first with only positive match values (extent of inclusion), and then with all the match values (both inclusion and exclusion).

Table

1. Each **row** of the spreadsheet provides summary results for a TrueAllele-inferred evidence genotype of a contributor to a biological evidence item.

2. The **columns** describe the contributor genotype as:

Evidence	A ‘request name' is an identifier that names a TrueAllele interpretation request. The identifier usually contains a case name, followed by an evidence item name, and may describe parameter settings as well. More information about the test conditions is found in the Request section.
Contributor	This field identifies which contributor to the mixture is being described.
N contrib	The total number of contributors assumed to be present in a mixture.
Weight	The inferred mixture weight for the specified contributor.
Std Dev	The standard deviation of that contributor's mixture weight.
KL	The average log(LR) statistic indicates to what extent the inferred contributor genotype differs from a population genotype.
References	Each succeeding column specifies a particular reference genotype.

3. Each match **entry** gives the likelihood ratio (LR) DNA match statistic between a pair of evidence (row) and reference (column) genotypes. The LR is displayed as a log(LR) value that gives the logarithm (or, powers of ten) of the LR.

The log(LR) value shown is the smallest one across the considered reference populations. The LR values are computed assuming a coancestry coefficient of 1%.

The LR is a nonprejudicial numerical assessment of the probative force of the specified DNA evidence for the hypothesis that a particular individual contributed their DNA to the biological evidence. The statistic can be read as saying "a match between the suspect and the evidence is (the LR value) times more probable than coincidence."

Item 12-9.5.1

Evidence	Contributor	N Contrib	Weight	Std Dev	KL	DT	TT
glove_ncon3_dgrd_200K	1	3	0.37	0.16	5.83	3.08	5.14
glove_ncon3_dgrd_200K	2	3	0.31	0.20	4.44	2.82	4.62
glove_ncon3_dgrd_200K	3	3	0.32	0.17	4.72	2.59	4.48
glove_ncon3_dgrd_200K_rep1	1	3	0.29	0.19	4.36	2.24	4.14
glove_ncon3_dgrd_200K_rep1	2	3	0.34	0.19	4.97	3.02	5.03
glove_ncon3_dgrd_200K_rep1	3	3	0.37	0.16	5.56	2.65	5.05
glove+TT_ncon3_dgrd_200K	2	3	0.28	0.14	5.66		
glove+TT_ncon3_dgrd_200K	3	3	0.29	0.16	5.45		
glove+TT_ncon3_dgrd_200K_rep1	2	3	0.30	0.15	5.53		
glove+TT_ncon3_dgrd_200K_rep1	3	3	0.29	0.16	5.15	0.29	
glove_ncon4_dgrd_200K	1	4	0.28	0.24	4.53	4.23	4.83
glove_ncon4_dgrd_200K	2	4	0.28	0.17	4.61	3.92	4.35
glove_ncon4_dgrd_200K	3	4	0.18	0.13	3.43	2.38	2.72
glove_ncon4_dgrd_200K	4	4	0.26	0.17	4.12	4.06	4.61
glove_ncon4_dgrd_200K_rep1	1	4	0.24	0.23	3.89	4.15	4.24
glove_ncon4_dgrd_200K_rep1	2	4	0.28	0.20	4.59	4.25	4.60
glove_ncon4_dgrd_200K_rep1	3	4	0.24	0.15	4.02	3.34	3.69
glove_ncon4_dgrd_200K_rep1	4	4	0.24	0.18	3.82	3.56	4.02
glove+TT_ncon4_dgrd_200K	2	4	0.25	0.17	4.26	2.61	
glove+TT_ncon4_dgrd_200K	3	4	0.26	0.18	4.13	3.36	
glove+TT_ncon4_dgrd_200K	4	4	0.24	0.14	4.07	2.36	
glove+TT_ncon4_dgrd_200K_rep1	2	4	0.23	0.15	4.84	0.47	
glove+TT_ncon4_dgrd_200K_rep1	3	4	0.22	0.19	3.93	1.77	
glove+TT_ncon4_dgrd_200K_rep1	4	4	0.19	0.21	3.14	1.71	
glove+TT_ncon4_dgrd_200K_rep2	2	4	0.24	0.18	4.08	2.55	
glove+TT_ncon4_dgrd_200K_rep2	3	4	0.24	0.16	4.19	1.98	
glove+TT_ncon4_dgrd_200K_rep2	4	4	0.24	0.22	3.76	2.72	
glove_ncon5_dgrd_200K	1	5	0.24	0.19	4.08	4.50	4.74
glove_ncon5_dgrd_200K	2	5	0.25	0.21	4.59	4.43	4.60
glove_ncon5_dgrd_200K	3	5	0.17	0.21	2.94	2.08	3.34
glove_ncon5_dgrd_200K	4	5	0.17	0.22	2.77	3.48	4.00
glove_ncon5_dgrd_200K	5	5	0.17	0.16	2.98	2.71	3.23
glove_ncon5_dgrd_200K_rep1	1	5	0.14	0.19	2.87	2.71	3.07
glove_ncon5_dgrd_200K_rep1	2	5	0.31	0.14	6.19	4.38	4.94
glove_ncon5_dgrd_200K_rep1	3	5	0.24	0.16	4.28	3.74	3.71
glove_ncon5_dgrd_200K_rep1	4	5	0.13	0.17	2.62	1.75	2.83
glove_ncon5_dgrd_200K_rep1	5	5	0.18	0.23	2.91	3.67	4.15
glove_ncon5_dgrd_200K_rep2	1	5	0.21	0.20	3.87	4.39	4.22
glove_ncon5_dgrd_200K_rep2	2	5	0.15	0.20	2.53	3.11	3.33
glove_ncon5_dgrd_200K_rep2	3	5	0.30	0.13	6.21	3.41	4.85
glove_ncon5_dgrd_200K_rep2	4	5	0.23	0.19	3.78	3.74	4.56
glove_ncon5_dgrd_200K_rep2	5	5	0.11	0.12	2.48	1.37	1.54
glove+TT_ncon5_dgrd_200K	2	5	0.22	0.18	3.96	3.35	
glove+TT_ncon5_dgrd_200K	3	5	0.26	0.16	4.83	3.85	
glove+TT_ncon5_dgrd_200K	4	5	0.15	0.18	3.03	1.60	
glove+TT_ncon5_dgrd_200K	5	5	0.19	0.17	3.36	2.95	
glove+TT_ncon5_dgrd_200K_rep1	2	5	0.18	0.13	3.43	2.84	
glove+TT_ncon5_dgrd_200K_rep1	3	5	0.13	0.15	2.71	1.90	
glove+TT_ncon5_dgrd_200K_rep1	4	5	0.26	0.16	4.92	3.25	
glove+TT_ncon5_dgrd_200K_rep1	5	5	0.17	0.19	2.90	2.60	
glove+TT_ncon5_dgrd_200K_rep2	2	5	0.19	0.16	3.33	2.78	
glove+TT_ncon5_dgrd_200K_rep2	3	5	0.18	0.19	3.20	3.66	
glove+TT_ncon5_dgrd_200K_rep2	4	5	0.14	0.12	2.77	1.97	
glove+TT_ncon5_dgrd_200K_rep2	5	5	0.25	0.14	5.14	2.98	

Item 12-9.5.1

Evidence	Contributor	N Contrib	Weight	Std Dev	KL	DT	TT
glove_ncon3_dgrd_200K	1	3	0.37	0.16	5.83	3.08	5.14
glove_ncon3_dgrd_200K	2	3	0.31	0.20	4.44	2.82	4.62
glove_ncon3_dgrd_200K	3	3	0.32	0.17	4.72	2.59	4.48
glove_ncon3_dgrd_200K_rep1	1	3	0.29	0.19	4.36	2.24	4.14
glove_ncon3_dgrd_200K_rep1	2	3	0.34	0.19	4.97	3.02	5.03
glove_ncon3_dgrd_200K_rep1	3	3	0.37	0.16	5.56	2.65	5.05
glove+TT_ncon3_dgrd_200K	2	3	0.28	0.14	5.66	-0.39	-7.92
glove+TT_ncon3_dgrd_200K	3	3	0.29	0.16	5.45	-0.49	-7.58
glove+TT_ncon3_dgrd_200K_rep1	2	3	0.30	0.15	5.53	-0.07	-6.71
glove+TT_ncon3_dgrd_200K_rep1	3	3	0.29	0.16	5.15	0.29	-6.92
glove_ncon4_dgrd_200K	1	4	0.28	0.24	4.53	4.23	4.83
glove_ncon4_dgrd_200K	2	4	0.28	0.17	4.61	3.92	4.35
glove_ncon4_dgrd_200K	3	4	0.18	0.13	3.43	2.38	2.72
glove_ncon4_dgrd_200K	4	4	0.26	0.17	4.12	4.06	4.61
glove_ncon4_dgrd_200K_rep1	1	4	0.24	0.23	3.89	4.15	4.24
glove_ncon4_dgrd_200K_rep1	2	4	0.28	0.20	4.59	4.25	4.60
glove_ncon4_dgrd_200K_rep1	3	4	0.24	0.15	4.02	3.34	3.69
glove_ncon4_dgrd_200K_rep1	4	4	0.24	0.18	3.82	3.56	4.02
glove+TT_ncon4_dgrd_200K	2	4	0.25	0.17	4.26	2.61	-2.34
glove+TT_ncon4_dgrd_200K	3	4	0.26	0.18	4.13	3.36	-1.98
glove+TT_ncon4_dgrd_200K	4	4	0.24	0.14	4.07	2.36	-2.08
glove+TT_ncon4_dgrd_200K_rep1	2	4	0.23	0.15	4.84	0.47	-6.04
glove+TT_ncon4_dgrd_200K_rep1	3	4	0.22	0.19	3.93	1.77	-4.43
glove+TT_ncon4_dgrd_200K_rep1	4	4	0.19	0.21	3.14	1.71	-4.10
glove+TT_ncon4_dgrd_200K_rep2	2	4	0.24	0.18	4.08	2.55	-3.07
glove+TT_ncon4_dgrd_200K_rep2	3	4	0.24	0.16	4.19	1.98	-3.13
glove+TT_ncon4_dgrd_200K_rep2	4	4	0.24	0.22	3.76	2.72	-2.72
glove_ncon5_dgrd_200K	1	5	0.24	0.19	4.08	4.50	4.74
glove_ncon5_dgrd_200K	2	5	0.25	0.21	4.59	4.43	4.60
glove_ncon5_dgrd_200K	3	5	0.17	0.21	2.94	2.08	3.34
glove_ncon5_dgrd_200K	4	5	0.17	0.22	2.77	3.48	4.00
glove_ncon5_dgrd_200K	5	5	0.17	0.16	2.98	2.71	3.23
glove_ncon5_dgrd_200K_rep1	1	5	0.14	0.19	2.87	2.71	3.07
glove_ncon5_dgrd_200K_rep1	2	5	0.31	0.14	6.19	4.38	4.94
glove_ncon5_dgrd_200K_rep1	3	5	0.24	0.16	4.28	3.74	3.71
glove_ncon5_dgrd_200K_rep1	4	5	0.13	0.17	2.62	1.75	2.83
glove_ncon5_dgrd_200K_rep1	5	5	0.18	0.23	2.91	3.67	4.15
glove_ncon5_dgrd_200K_rep2	1	5	0.21	0.20	3.87	4.39	4.22
glove_ncon5_dgrd_200K_rep2	2	5	0.15	0.20	2.53	3.11	3.33
glove_ncon5_dgrd_200K_rep2	3	5	0.30	0.13	6.21	3.41	4.85
glove_ncon5_dgrd_200K_rep2	4	5	0.23	0.19	3.78	3.74	4.56
glove_ncon5_dgrd_200K_rep2	5	5	0.11	0.12	2.48	1.37	1.54
glove+TT_ncon5_dgrd_200K	2	5	0.22	0.18	3.96	3.35	-0.68
glove+TT_ncon5_dgrd_200K	3	5	0.26	0.16	4.83	3.85	-0.33
glove+TT_ncon5_dgrd_200K	4	5	0.15	0.18	3.03	1.60	-1.63
glove+TT_ncon5_dgrd_200K	5	5	0.19	0.17	3.36	2.95	-0.71
glove+TT_ncon5_dgrd_200K_rep1	2	5	0.18	0.13	3.43	2.84	-1.73
glove+TT_ncon5_dgrd_200K_rep1	3	5	0.13	0.15	2.71	1.90	-2.59
glove+TT_ncon5_dgrd_200K_rep1	4	5	0.26	0.16	4.92	3.25	-1.47
glove+TT_ncon5_dgrd_200K_rep1	5	5	0.17	0.19	2.90	2.60	-1.43
glove+TT_ncon5_dgrd_200K_rep2	2	5	0.19	0.16	3.33	2.78	-1.13
glove+TT_ncon5_dgrd_200K_rep2	3	5	0.18	0.19	3.20	3.66	-1.31
glove+TT_ncon5_dgrd_200K_rep2	4	5	0.14	0.12	2.77	1.97	-2.29
glove+TT_ncon5_dgrd_200K_rep2	5	5	0.25	0.14	5.14	2.98	-2.34

Locus Table

A locus table is provided for each reported match. The table gives the log(LR) values of individual loci. A row corresponds to the locus indicated in the first column. Each subsequent column gives locus statistics for a different ethnic population.

Total	The sum of the log(LR) values.
Joint	The total likelihood ratio as a linear number.
Words	The total likelihood ratio as a descriptive phrase.

Item 12-9.5.1 v. suspect 12-1.1.1
glove_ncon5_dgrd_200K_rep1 contributor 2 vs. DT

locus	US_BLK_FBI	US_CAU_FBI	US_HIS_FBI
CSF1PO	-0.2434	-0.3113	-0.2955
D13S317	1.2030	1.0683	1.1417
D16S539	0.3909	0.4144	0.2238
D18S51	-0.5700	-0.6719	-0.6789
D19S433	0.2423	-0.1830	-0.0843
D21S11	1.2959	1.1659	1.1346
D2S1338	0.7047	0.4907	0.3336
D3S1358	0.4481	0.5142	0.4839
D5S818	0.1746	-0.0033	-0.0092
D7S820	0.8019	0.7225	0.6264
D8S1179	0.2818	0.2431	0.2616
FGA	0.9375	0.9075	0.9962
TH01	-0.2987	-0.3289	-0.3526
TPOX	0.7240	0.4284	0.3520
vWA	0.3817	0.1984	0.2491
Total	6.4742	4.6550	4.3824
Joint	2980104	45183	24122
Words	2.98 million	45.2 thousand	24.1 thousand

Item 12-9.5.1 v. suspect 15-1.1
glove_ncon5_dgrd_200K_rep2 contributor 3 vs. TT

locus	US_BLK_FBI	US_CAU_FBI	US_HIS_FBI
CSF1PO	-0.0265	-0.1177	-0.1102
D13S317	0.8998	0.7366	0.8035
D16S539	0.7480	0.7692	0.5883
D18S51	-0.8001	-0.9058	-0.9101
D19S433	0.9892	0.5582	0.6409
D21S11	0.9632	0.8276	0.7837
D2S1338	0.6617	0.4536	0.2812
D3S1358	0.5477	0.6334	0.5739
D5S818	0.0456	-0.1382	-0.1342
D7S820	0.7444	0.6904	0.6387
D8S1179	0.1607	0.1536	0.1695
FGA	0.8953	0.8777	0.9481
TH01	-0.0272	-0.0594	-0.0694
TPOX	0.8501	0.5479	0.4457
vWA	0.3410	0.1634	0.1993
Total	6.9929	5.1904	4.8488
Joint	9837756	155040	70605
Words	9.84 million	155 thousand	70.6 thousand

Specificity

The specificity chart and tables show how a reported match between evidence and a subject genotype relates to matches between the evidence and random genotypes.

Chart

graph	The histogram displays the match statistic log(LR) distribution between the inferred genotype and random non-contributor genotypes for a given reference population
x axis	log(LR) values
y axis	Number of times each log(LR) value appears when comparing the inferred genotype to the non-contributor genotypes (e.g. counts)
arrow	Reported match log(LR) value

Statistics table

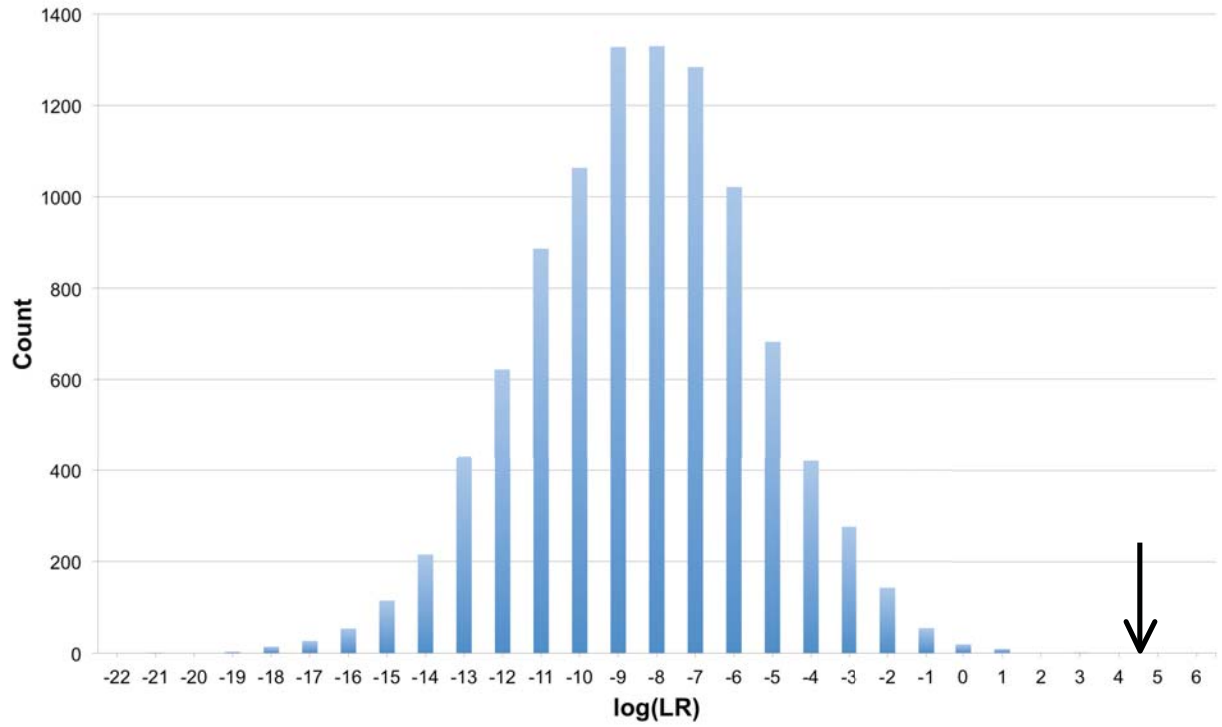
N	Number of match statistics calculated for the distribution
minimum	Smallest match statistic between the inferred genotype and the random non-contributor genotypes
mean	Average match statistic
median	Middle match statistic
maximum	Largest match statistic
std dev	Standard deviation of the distribution
positive	Number of log(LR) values greater than zero
mu	Mean of the normal curve modeled to the distribution
sigma	Standard deviation of a normal curve modeled to the distribution

Item table

item	Name or number of the genotype; typically a case reference
LR	Likelihood ratio value between the inferred genotype and the item, relative to a reference population
log(LR)	Logarithm of the LR (e.g. “number of zeroes”)
z-score	Number of standard deviations the item log(LR) value is from the mean
p-value	Probability of a non-contributor having a match statistic equal to or greater than the item log(LR)

Item 12-9.5.1 and suspect 12-1.1.1

Comparison was made between the reported evidence genotype and 10,000 randomly generated genotypes from the United States FBI Caucasian population to calculate the LR match statistics.

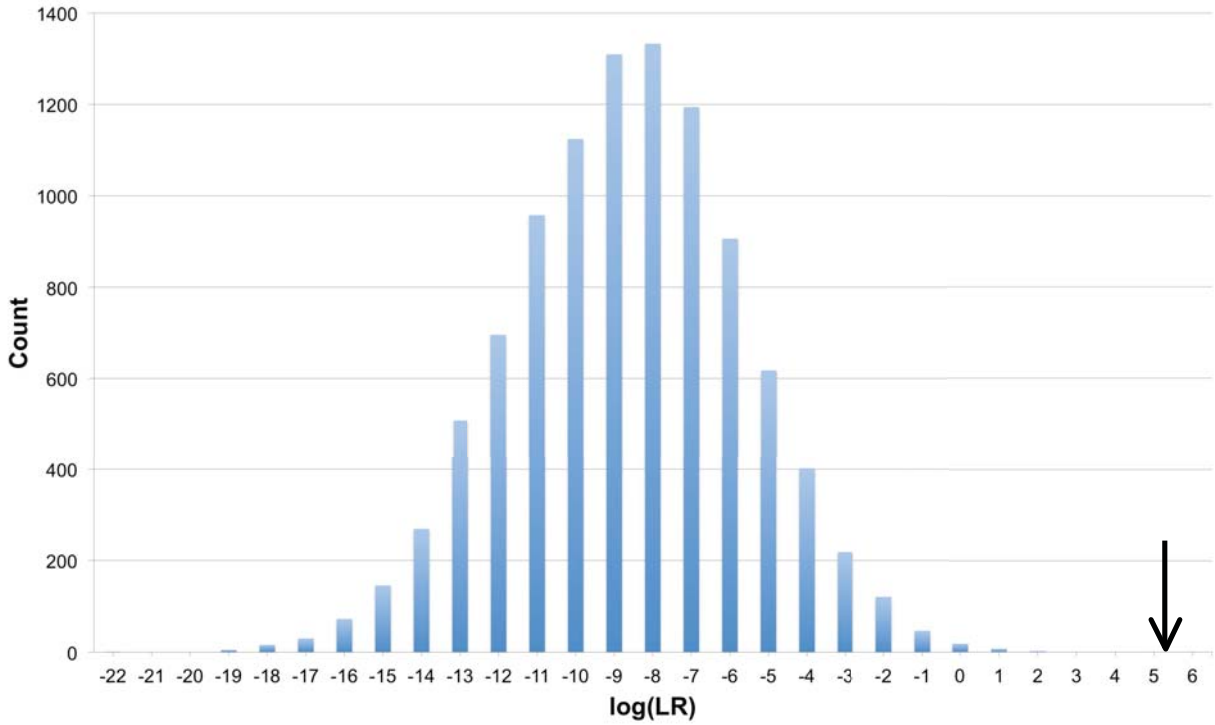


stat	value
N =	10000
minimum	-20.3192
mean	-7.8789
median	-7.8219
maximum	3.0113
std dev	2.9606
positive	29
mu	-7.8789
sigma	2.9604

item	LR	log(LR)	z-score	p-value
12-1.1.1	45.2 thousand	4.65	4.2338	1.15×10^{-5}

Item 12-9.5.1 and suspect 15-1.1

Comparison was made between the reported evidence genotype and 10,000 randomly generated genotypes from the United States FBI Caucasian population to calculate the LR match statistics.



stat	value
N =	10000
minimum	-21.1854
mean	-8.1581
median	-8.1022
maximum	2.5734
std dev	3.0017
positive	27
mu	-8.1581
sigma	3.0015

item	LR	log(LR)	z-score	p-value
15-1.1	155 thousand	5.19	4.4473	4.35×10^{-6}